

Asn Thr Thr Ala Ala Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala  
 290 295 300  
 Val Phe Ala Gly Gly Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn  
 305 310 315 320  
 Leu Leu Ala Ser Val Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly  
 325 330 335  
 Leu Leu Ile Ala Gly Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys  
 340 345 350  
 Ser Val Lys Ala Val Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu  
 355 360 365  
 Glu Asp Glu Glu Glu His Val Glu Glu Glu Val Asp Glu Glu Glu Glu  
 370 375 380  
 Glu Val Glu Glu Gly Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp  
 385 390 395 400  
 Pro Glu Glu Asn Pro Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr  
 405 410 415  
 Glu Thr Glu Ala Glu Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg  
 420 425 430

&lt;210&gt; 1097

&lt;211&gt; 603

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(580)

&lt;223&gt; RXC02665

&lt;400&gt; 1097

caaggcgacc caatggcggtt taaagtaaca acccccattg atatgatgct ggcacaacgc 60

atcaccgacg aagccgaacc cacaatatatt gaggtaccag gtg act aac cca atc 115  
 Val Thr Asn Pro Ile  
 1 5

atc ccc cgc gta gga atc gcc aca gac gcc cac caa atc gaa gcg gga 163  
 Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His Gln Ile Glu Ala Gly  
 10 15 20

aaa ccc tgc tgg atc gcc tgc ctc ctc ttt gaa ggc gtc gac ggc tgc 211  
 Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu Gly Val Asp Gly Cys  
 25 30 35

gaa ggc cac tcc gac ggt gat gtt gta gct cat gca att gtg gat gct 259  
 Glu Gly His Ser Asp Gly Asp Val Val Ala His Ala Ile Val Asp Ala  
 40 45 50

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ctc ctt tct gcc tct ggt ctg ggg gat ttg ggc tct ttc gtt ggt gtg 307
Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly Ser Phe Val Gly Val
    55                60                65

ggg aga cct gaa tac gat ggt gtt tct ggt aca cag ttg ttg aag gaa 355
Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr Gln Leu Leu Lys Glu
    70                75                80                85

gtt cgg gag ctg ctt tcg gca cac ggg tac gtc att gga aat gtc gcc 403
Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val Ile Gly Asn Val Ala
                90                95                100

gcc caa ctg gtt ggc caa acc ccc aaa ttt gga ccc cgc cgc gaa gaa 451
Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly Pro Arg Arg Glu Glu
                105                110                115

gca caa caa gtc atc tcc gaa atc atc ggc gca cca tgc tca ctg tct 499
Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala Pro Cys Ser Leu Ser
                120                125                130

gcc acc acc act gat cac atg gga ttc act ggt cgc agc gag ggt cgt 547
Ala Thr Thr Thr Asp His Met Gly Phe Thr Gly Arg Ser Glu Gly Arg
                135                140                145

gca tcg gta gca acg gca gtg gtg tgg aag gct taagttttct gtagggattg 600
Ala Ser Val Ala Thr Ala Val Val Trp Lys Ala
150                155                160

ggc 603

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&lt;210&gt; 1098

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1098

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Val Thr Asn Pro Ile Ile Pro Arg Val Gly Ile Ala Thr Asp Ala His
    1                5                10                15

Gln Ile Glu Ala Gly Lys Pro Cys Trp Ile Ala Cys Leu Leu Phe Glu
                20                25                30

Gly Val Asp Gly Cys Glu Gly His Ser Asp Gly Asp Val Val Ala His
                35                40                45

Ala Ile Val Asp Ala Leu Leu Ser Ala Ser Gly Leu Gly Asp Leu Gly
    50                55                60

Ser Phe Val Gly Val Gly Arg Pro Glu Tyr Asp Gly Val Ser Gly Thr
    65                70                75                80

Gln Leu Leu Lys Glu Val Arg Glu Leu Leu Ser Ala His Gly Tyr Val
                85                90                95

Ile Gly Asn Val Ala Ala Gln Leu Val Gly Gln Thr Pro Lys Phe Gly
                100                105                110

Pro Arg Arg Glu Glu Ala Gln Gln Val Ile Ser Glu Ile Ile Gly Ala
    115                120                125

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Pro	Cys	Ser	Leu	Ser	Ala	Thr	Thr	Thr	Asp	His	Met	Gly	Phe	Thr	Gly
130						135					140				
Arg	Ser	Glu	Gly	Arg	Ala	Ser	Val	Ala	Thr	Ala	Val	Val	Trp	Lys	Ala
145					150					155					160

&lt;210&gt; 1099

&lt;211&gt; 1689

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1666)

&lt;223&gt; RXC02770

&lt;400&gt; 1099

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tcgccggggc aaaaaccgta taattacagt cctattacga ttcggggaaa ggctgggtac 60
ttcacacatg ttgtttcgga agtcacgcag cgcggtaatc atg ttg gtt gca gcg 115
                                         Met Leu Val Ala Ala
                                         1                               5

tta gtg atg aca agc tgt ggt gat ggg gaa ccg gaa cca acc agc cac 163
Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro Glu Pro Thr Ser His
                               10                               15                               20

caa aca agc ctt ttc ggc tac gca gtt aac tct tcg ctg gct aca acc 211
Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser Ser Leu Ala Thr Thr
                               25                               30                               35

aac gcg gcg tcg ctg ttg gga gtg gct aat gat gct ggt ctt ttg gct 259
Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp Ala Gly Leu Leu Ala
                               40                               45                               50

gcc aga gtg tat ccg ggt gtg tat gtt cag ggt cct tct ggg cag atg 307
Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly Pro Ser Gly Gln Met
                               55                               60                               65

att ccc aac act gat ctt gct tcc acg cag gta ttg ccg ggt att aac 355
Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val Leu Pro Gly Ile Asn
                               70                               75                               80                               85

cgc cag gtg att tac act atc aat gaa gat gcc acc tac tca gat ggt 403
Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala Thr Tyr Ser Asp Gly
                               90                               95                               100

cag cct gtg gtg tgt gat gat ttt ctg ctc tct gcg aca gct ggg cag 451
Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser Ala Thr Ala Gly Gln
                               105                               110                               115

atg ccg gaa ctg ttc cag tcc cat gtg cca ttg acc tcg cag att gag 499
Met Pro Glu Leu Phe Gln Ser His Val Pro Leu Thr Ser Gln Ile Glu
                               120                               125                               130

cga gtg gac tgt gta tct ggt tct aaa gta gcc acc gtg gtg ttc aag 547
Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala Thr Val Val Phe Lys

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135	140	145	
gaa gac ctc ggt gag cgt tgg cgt tat ctt ttt gag cag ggc gat ttg			595
Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe Glu Gln Gly Asp Leu			
150	155	160	165
ttg cca gcc cat gcc gtt gct tcc aaa gca ggt atg acc ttg gag gag			643
Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly Met Thr Leu Glu Glu			
	170	175	180
ctt aat cag gcg ttg aag gat aag gat cct gaa gcg ttg act gaa cct			691
Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu Ala Leu Thr Glu Pro			
	185	190	195
gct cgt gtg tgg agc gaa ggt ttc cag ctg tcc cag ttt gat cca gag			739
Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser Gln Phe Asp Pro Glu			
	200	205	210
ctg cag acg gct ttt ggc cgc tac aag gtg gat tct gtg ggt gaa ttc			787
Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp Ser Val Gly Glu Phe			
	215	220	225
ggc gaa gtc aag ctg gta cgc aat gag ttt tac agt ggc gac cag gcg			835
Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr Ser Gly Asp Gln Ala			
	230	235	240
gtt gaa gca gaa atc acg atg tgg cct aaa ggc tcg gat ctc agc gcc			883
Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly Ser Asp Leu Ser Ala			
	250	255	260
att gcg gat aat gga aac ctt cag atc gca cat gtt gtg gcg tgg gag			931
Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His Val Val Ala Trp Glu			
	265	270	275
agc gag cgc tgg gta aat cgc gat gac cca ttg aat cct tat gac att			979
Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu Asn Pro Tyr Asp Ile			
	280	285	290
aag gaa gag gtc ggt gtt ttg act gag cag ctc acc ttg gcc agt gcc			
1027			
Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu Thr Leu Ala Ser Ala			
	295	300	305
ggt gtg ttt tac gct gcg gag gcc cgg cag gcg ttt gcg gcc tgc gtt			
1075			
Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala Phe Ala Ala Cys Val			
	310	315	320
gac cag gaa gcg gtg gct gcg gcg tcg tca agc atc tct gga atc gat			
1123			
Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser Ile Ser Gly Ile Asp			
	330	335	340
gtg cct gcc gta ggt gtg cac tcg gtg cgt cac caa aat ccg gtc gtg			
1171			
Val Pro Ala Val Gly Val His Ser Val Arg His Gln Asn Pro Val Val			
	345	350	355
cac caa atc ggt gat ctg cca gca cag cac atg gcg gtg gat att aat			
1219			
His Gln Ile Gly Asp Leu Pro Ala Gln His Met Ala Val Asp Ile Asn			

360                                      365                                      370  
 gcc gca tca gcg ttg gcg ggt caa tcc atc cgc att ggc tac gac gga  
 1267  
 Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg Ile Gly Tyr Asp Gly  
       375                                      380                                      385  
 ccc gat gag cgc aag gct gca atg gtg gag gcg att cgc caa agt tgt  
 1315  
 Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala Ile Arg Gln Ser Cys  
 390                                      395                                      400                                      405  
 gag cct gcc ggt atc acc gtt atc gat gcg tcg cag gag gct gtt agt  
 1363  
 Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser Gln Glu Ala Val Ser  
                                     410                                      415                                      420  
 ctt aat gat ctc agt cga acc gaa gtc agt gaa tgg ggc tat gag cag  
 1411  
 Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu Trp Gly Tyr Glu Gln  
                                     425                                      430                                      435  
 tac ttc gaa ggg aca ctt gac gct gtt ctg cgt aca gtg gat cca cat  
 1459  
 Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg Thr Val Asp Pro His  
                                     440                                      445                                      450  
 cgg gag tat gaa aat gcc aat acc att gga act gat gcg gag tcg acg  
 1507  
 Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr Asp Ala Glu Ser Thr  
                                     455                                      460                                      465  
 agg cgc act gaa gaa caa ttg tgg gct gaa gtc cca tca att cca cta  
 1555  
 Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val Pro Ser Ile Pro Leu  
 470                                      475                                      480                                      485  
 gca gcg caa ccc cga gtg ttt gtg ata gat cgc aca gtc ggt aac gtt  
 1603  
 Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg Thr Val Gly Asn Val  
                                     490                                      495                                      500  
 gtt gtt aat aca gac cta gcc ggt atc gga tgg aac atg gac cgt tgg  
 1651  
 Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp Asn Met Asp Arg Trp  
                                     505                                      510                                      515  
 tcc aga agt gag gaa taagtagtga gcgaacaagc tct  
 1689  
 Ser Arg Ser Glu Glu  
                                     520

&lt;210&gt; 1100

&lt;211&gt; 522

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1100

Met Leu Val Ala Ala Leu Val Met Thr Ser Cys Gly Asp Gly Glu Pro  
       1                                      5                                      10                                      15

Glu Pro Thr Ser His Gln Thr Ser Leu Phe Gly Tyr Ala Val Asn Ser  
 20 25 30  
 Ser Leu Ala Thr Thr Asn Ala Ala Ser Leu Leu Gly Val Ala Asn Asp  
 35 40 45  
 Ala Gly Leu Leu Ala Ala Arg Val Tyr Pro Gly Val Tyr Val Gln Gly  
 50 55 60  
 Pro Ser Gly Gln Met Ile Pro Asn Thr Asp Leu Ala Ser Thr Gln Val  
 65 70 75 80  
 Leu Pro Gly Ile Asn Arg Gln Val Ile Tyr Thr Ile Asn Glu Asp Ala  
 85 90 95  
 Thr Tyr Ser Asp Gly Gln Pro Val Val Cys Asp Asp Phe Leu Leu Ser  
 100 105 110  
 Ala Thr Ala Gly Gln Met Pro Glu Leu Phe Gln Ser His Val Pro Leu  
 115 120 125  
 Thr Ser Gln Ile Glu Arg Val Asp Cys Val Ser Gly Ser Lys Val Ala  
 130 135 140  
 Thr Val Val Phe Lys Glu Asp Leu Gly Glu Arg Trp Arg Tyr Leu Phe  
 145 150 155 160  
 Glu Gln Gly Asp Leu Leu Pro Ala His Ala Val Ala Ser Lys Ala Gly  
 165 170 175  
 Met Thr Leu Glu Glu Leu Asn Gln Ala Leu Lys Asp Lys Asp Pro Glu  
 180 185 190  
 Ala Leu Thr Glu Pro Ala Arg Val Trp Ser Glu Gly Phe Gln Leu Ser  
 195 200 205  
 Gln Phe Asp Pro Glu Leu Gln Thr Ala Phe Gly Pro Tyr Lys Val Asp  
 210 215 220  
 Ser Val Gly Glu Phe Gly Glu Val Lys Leu Val Arg Asn Glu Phe Tyr  
 225 230 235 240  
 Ser Gly Asp Gln Ala Val Glu Ala Glu Ile Thr Met Trp Pro Lys Gly  
 245 250 255  
 Ser Asp Leu Ser Ala Ile Ala Asp Asn Gly Asn Leu Gln Ile Ala His  
 260 265 270  
 Val Val Ala Trp Glu Ser Glu Pro Trp Val Asn Arg Asp Asp Pro Leu  
 275 280 285  
 Asn Pro Tyr Asp Ile Lys Glu Glu Val Gly Val Leu Thr Glu Gln Leu  
 290 295 300  
 Thr Leu Ala Ser Ala Gly Val Phe Tyr Ala Ala Glu Ala Arg Gln Ala  
 305 310 315 320  
 Phe Ala Ala Cys Val Asp Gln Glu Ala Val Ala Ala Ala Ser Ser Ser  
 325 330 335

Ile Ser Gly Ile Asp Val Pro Ala Val Gly Val His Ser Val Arg His  
 340 345 350

Gln Asn Pro Val Val His Gln Ile Gly Asp Leu Pro Ala Gln His Met  
 355 360 365

Ala Val Asp Ile Asn Ala Ala Ser Ala Leu Ala Gly Gln Ser Ile Arg  
 370 375 380

Ile Gly Tyr Asp Gly Pro Asp Glu Arg Lys Ala Ala Met Val Glu Ala  
 385 390 395 400

Ile Arg Gln Ser Cys Glu Pro Ala Gly Ile Thr Val Ile Asp Ala Ser  
 405 410 415

Gln Glu Ala Val Ser Leu Asn Asp Leu Ser Arg Thr Glu Val Ser Glu  
 420 425 430

Trp Gly Tyr Glu Gln Tyr Phe Glu Gly Thr Leu Asp Ala Val Leu Arg  
 435 440 445

Thr Val Asp Pro His Arg Glu Tyr Glu Asn Ala Asn Thr Ile Gly Thr  
 450 455 460

Asp Ala Glu Ser Thr Arg Arg Thr Glu Glu Gln Leu Trp Ala Glu Val  
 465 470 475 480

Pro Ser Ile Pro Leu Ala Ala Gln Pro Arg Val Phe Val Ile Asp Arg  
 485 490 495

Thr Val Gly Asn Val Val Val Asn Thr Asp Leu Ala Gly Ile Gly Trp  
 500 505 510

Asn Met Asp Arg Trp Ser Arg Ser Glu Glu  
 515 520

<210> 1101  
 <211> 408  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(385)  
 <223> RXC02238

<400> 1101  
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ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115  
 Val Thr Asn Val Ser  
 1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163  
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile  
 10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211  
 Thr Ala Pro Pro Ile Asp Glu Leu Asp Lys Val Thr Ser Lys Tyr  
 25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259  
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe  
           40                          45                          50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307  
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val  
           55                          60                          65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355  
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile  
           70                          75                          80                          85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405  
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
                           90                          95

cac 408

<210> 1102

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 1102

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp  
           1                          5                          10                          15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys  
                           20                          25                          30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg  
           35                          40                          45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe  
           50                          55                          60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile  
           65                          70                          75                          80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
                           85                          90                          95

<210> 1103

<211> 1298

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1275)

<223> RXC01946

<400> 1103

atc cgc aag tac tcc agg ctc gag gaa caa ttc cag tcg ctc ggc ggc 48  
 Ile Arg Lys Tyr Ser Arg Leu Glu Glu Gln Phe Gln Ser Leu Gly Gly  
           1                          5                          10                          15

tac gaa gct gac gcc gaa gca gcc cag atc tgc gac aac ctc ggc ctc 96



Tyr	Glu	Ala	Asp	Ala	Glu	Ala	Ala	Gln	Ile	Cys	Asp	Asn	Leu	Gly	Leu	
			20					25					30			
gag	gca	cgc	atc	ctc	gac	cag	cag	ctt	aaa	acc	ctg	tcc	ggc	ggc	cag	144
Glu	Ala	Arg	Ile	Leu	Asp	Gln	Gln	Leu	Lys	Thr	Leu	Ser	Gly	Gly	Gln	
		35					40					45				
cgc	cgc	cgc	gtc	gag	ttg	gcg	cag	atc	ctc	ttc	gcc	gcc	acc	aac	ggc	192
Arg	Arg	Arg	Val	Glu	Leu	Ala	Gln	Ile	Leu	Phe	Ala	Ala	Thr	Asn	Gly	
		50				55					60					
tcc	ggc	aaa	tca	aaa	acc	aca	ttg	ctt	ctc	gac	gag	ccc	acc	aac	cac	240
Ser	Gly	Lys	Ser	Lys	Thr	Thr	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	His	
	65				70				75						80	
ttg	gac	gca	gac	tcg	atc	acc	tgg	ctc	cgt	gac	ttc	ctg	gcg	aag	cac	288
Leu	Asp	Ala	Asp	Ser	Ile	Thr	Trp	Leu	Arg	Asp	Phe	Leu	Ala	Lys	His	
				85					90					95		
gaa	ggt	gga	ctg	atc	atg	att	tcg	cac	gac	gtc	gaa	ctg	ctt	ggc	gcc	336
Glu	Gly	Gly	Leu	Ile	Met	Ile	Ser	His	Asp	Val	Glu	Leu	Leu	Gly	Ala	
			100					105					110			
gta	tgt	aac	aag	att	tgg	tac	ctc	gac	gca	gta	cgc	agc	gaa	gcc	gat	384
Val	Cys	Asn	Lys	Ile	Trp	Tyr	Leu	Asp	Ala	Val	Arg	Ser	Glu	Ala	Asp	
		115					120					125				
gtc	tac	aac	atg	ggc	ttt	agc	aaa	tac	gtc	gat	gca	cgt	gca	ctc	gat	432
Val	Tyr	Asn	Met	Gly	Phe	Ser	Lys	Tyr	Val	Asp	Ala	Arg	Ala	Leu	Asp	
	130					135					140					
gaa	gca	cgc	cga	cgc	cgt	gag	cgc	gca	aac	gcc	gaa	aag	aag	gcc	gga	480
Glu	Ala	Arg	Arg	Arg	Arg	Glu	Arg	Ala	Asn	Ala	Glu	Lys	Lys	Ala	Gly	
	145				150				155						160	
gcc	ctc	aag	gac	cag	gct	gca	cgc	ctc	ggc	gcg	aaa	gca	acc	aag	gct	528
Ala	Leu	Lys	Asp	Gln	Ala	Ala	Arg	Leu	Gly	Ala	Lys	Ala	Thr	Lys	Ala	
				165					170					175		
gcc	gca	gct	aag	cag	atg	atc	gcc	cgt	gcg	gaa	cga	atg	atc	gac	aac	576
Ala	Ala	Ala	Lys	Gln	Met	Ile	Ala	Arg	Ala	Glu	Arg	Met	Ile	Asp	Asn	
			180				185						190			
ctc	gac	gaa	atc	cgc	gta	gct	gac	cgc	gcc	gcc	aac	atc	gtt	ttc	cca	624
Leu	Asp	Glu	Ile	Arg	Val	Ala	Asp	Arg	Ala	Ala	Asn	Ile	Val	Phe	Pro	
		195				200					205					
gaa	cca	gca	ccc	tgt	gga	aaa	acc	cca	ctc	aac	gcc	aag	ggc	ctg	acc	672
Glu	Pro	Ala	Pro	Cys	Gly	Lys	Thr	Pro	Leu	Asn	Ala	Lys	Gly	Leu	Thr	
	210					215					220					
aag	atg	tac	ggc	tcc	ctc	gaa	gtc	ttc	gcc	ggc	gtc	gac	cta	gcc	atc	720
Lys	Met	Tyr	Gly	Ser	Leu	Glu	Val	Phe	Ala	Gly	Val	Asp	Leu	Ala	Ile	
	225				230					235					240	
gac	aaa	ggc	tcc	cgc	gta	gtc	gtc	ctc	gga	ttc	aac	ggc	gca	ggc	aaa	768
Asp	Lys	Gly	Ser	Arg	Val	Val	Val	Leu	Gly	Phe	Asn	Gly	Ala	Gly	Lys	
				245					250					255		
acc	acc	ctg	ctc	aaa	ctc	ctc	gcc	ggc	gtg	gaa	cgc	acc	gac	ggc	gaa	816
Thr	Thr	Leu	Leu	Lys	Leu	Leu	Ala	Gly	Val	Glu	Arg	Thr	Asp	Gly	Glu	

260	265	270	
ggc ggc atc gtc acc gga tac ggc ctc aaa atc ggc tac ttc gcc cag			864
Gly Gly Ile Val Thr Gly Tyr	Gly Leu Lys Ile Gly Tyr	Phe Ala Gln	
275	280	285	
gaa cac gac acc atc gac ccc gac aaa tcc gtc tgg caa aac acc atc			912
Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile			
290	295	300	
gaa gcc tgc gcc gac gcc gac caa caa agc ctc cgc agc ctc ctc gga			960
Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly			
305	310	315	320
tcc ttc atg ttc tcc ggc gaa caa ctc gac caa cca gca gga aca ctc			
1008			
Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu			
	325	330	335
tcc ggc ggt gaa aaa acc cgc ctc gca ctg gcc acc ctc gtg tcc tcc			
1056			
Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser			
	340	345	350
cgc gca aac gtc ctg ctt ctc gac gag ccc acc aac aac ctt gac ccg			
1104			
Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro			
	355	360	365
atc tcc cgc gaa cag gtc ctc gac gca ctg cgc acc tac acc ggc gca			
1152			
Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala			
	370	375	380
gtc gtc ctg gtt acc cac gac ccg ggt gca gtc aag gcc ctt gag cca			
1200			
Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro			
385	390	395	400
gaa cgc gtc atc gtg ctt cct gat ggc acc gag gat ctt tgg aat gat			
1248			
Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp			
	405	410	415
cag tac atg gaa atc gtg gaa ttg gcg taggttctaa ggctgtttat			
1295			
Gln Tyr Met Glu Ile Val Glu Leu Ala			
	420	425	
gct			
1298			

&lt;210&gt; 1104

&lt;211&gt; 425

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1104

Ile	Arg	Lys	Tyr	Ser	Arg	Leu	Glu	Glu	Gln	Phe	Gln	Ser	Leu	Gly	Gly
1				5					10					15	

Tyr Glu Ala Asp Ala Glu Ala Ala Gln Ile Cys Asp Asn Leu Gly Leu  
 20 25 30  
 Glu Ala Arg Ile Leu Asp Gln Gln Leu Lys Thr Leu Ser Gly Gly Gln  
 35 40 45  
 Arg Arg Arg Val Glu Leu Ala Gln Ile Leu Phe Ala Ala Thr Asn Gly  
 50 55 60  
 Ser Gly Lys Ser Lys Thr Thr Leu Leu Leu Asp Glu Pro Thr Asn His  
 65 70 75 80  
 Leu Asp Ala Asp Ser Ile Thr Trp Leu Arg Asp Phe Leu Ala Lys His  
 85 90 95  
 Glu Gly Gly Leu Ile Met Ile Ser His Asp Val Glu Leu Leu Gly Ala  
 100 105 110  
 Val Cys Asn Lys Ile Trp Tyr Leu Asp Ala Val Arg Ser Glu Ala Asp  
 115 120 125  
 Val Tyr Asn Met Gly Phe Ser Lys Tyr Val Asp Ala Arg Ala Leu Asp  
 130 135 140  
 Glu Ala Arg Arg Arg Arg Glu Arg Ala Asn Ala Glu Lys Lys Ala Gly  
 145 150 155 160  
 Ala Leu Lys Asp Gln Ala Ala Arg Leu Gly Ala Lys Ala Thr Lys Ala  
 165 170 175  
 Ala Ala Ala Lys Gln Met Ile Ala Arg Ala Glu Arg Met Ile Asp Asn  
 180 185 190  
 Leu Asp Glu Ile Arg Val Ala Asp Arg Ala Ala Asn Ile Val Phe Pro  
 195 200 205  
 Glu Pro Ala Pro Cys Gly Lys Thr Pro Leu Asn Ala Lys Gly Leu Thr  
 210 215 220  
 Lys Met Tyr Gly Ser Leu Glu Val Phe Ala Gly Val Asp Leu Ala Ile  
 225 230 235 240  
 Asp Lys Gly Ser Arg Val Val Val Leu Gly Phe Asn Gly Ala Gly Lys  
 245 250 255  
 Thr Thr Leu Leu Lys Leu Leu Ala Gly Val Glu Arg Thr Asp Gly Glu  
 260 265 270  
 Gly Gly Ile Val Thr Gly Tyr Gly Leu Lys Ile Gly Tyr Phe Ala Gln  
 275 280 285  
 Glu His Asp Thr Ile Asp Pro Asp Lys Ser Val Trp Gln Asn Thr Ile  
 290 295 300  
 Glu Ala Cys Ala Asp Ala Asp Gln Gln Ser Leu Arg Ser Leu Leu Gly  
 305 310 315 320  
 Ser Phe Met Phe Ser Gly Glu Gln Leu Asp Gln Pro Ala Gly Thr Leu  
 325 330 335

Ser Gly Gly Glu Lys Thr Arg Leu Ala Leu Ala Thr Leu Val Ser Ser  
 340 345 350

Arg Ala Asn Val Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Pro  
 355 360 365

Ile Ser Arg Glu Gln Val Leu Asp Ala Leu Arg Thr Tyr Thr Gly Ala  
 370 375 380

Val Val Leu Val Thr His Asp Pro Gly Ala Val Lys Ala Leu Glu Pro  
 385 390 395 400

Glu Arg Val Ile Val Leu Pro Asp Gly Thr Glu Asp Leu Trp Asn Asp  
 405 410 415

Gln Tyr Met Glu Ile Val Glu Leu Ala  
 420 425

<210> 1105

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXN03171

<400> 1105

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cggtcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115  
 Met Asp Ile Thr Ile  
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403  
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451

Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
 150 155 160 165

gac gca ttg gcg gaa tct 613  
 Asp Ala Leu Ala Glu Ser  
 170

&lt;210&gt; 1106

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1106

Met Asp Ile Thr Ile Val Asn His Pro Leu Val Ala Ser Arg Leu Thr  
 1 5 10 15

Leu Leu Arg Asp Glu Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala  
 20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu  
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr  
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu  
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly  
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr  
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val  
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu  
 130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser  
 145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser  
 165 170

&lt;210&gt; 1107

<211> 613  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(613)  
 <223> FRXA02857

<400> 1107  
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cggtcttctt ctgggcggca atgatttaac atgtgaagct atg gac atc acc atc 115  
 Met Asp Ile Thr Ile  
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163  
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu  
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211  
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala  
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259  
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp  
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307  
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro  
 55 60 65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355  
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro  
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403  
 Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala  
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451  
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro  
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499  
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala  
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547  
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly  
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595  
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val  
 150 155 160 165

gac gca ttg gcg gaa tct 613  
 Asp Ala Leu Ala Glu Ser  
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<400> 1108																
Met	Asp	Ile	Thr	Ile	Val	Asn	His	Pro	Leu	Val	Ala	Ser	Arg	Leu	Thr	
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Leu	Leu	Arg	Asp	Glu	Arg	Ser	Asp	Asn	Ala	Ala	Phe	Arg	Ala	Ala	Ala	
			20					25					30			
Asn	Asp	Leu	Gly	Ala	Met	Leu	Ile	Tyr	Glu	Ala	Ser	Arg	Asp	Leu	Glu	
		35					40					45				
Val	Glu	His	Phe	Asp	Thr	Lys	Thr	Pro	Val	Ala	Met	Ala	Glu	Gly	Thr	
	50					55					60					
Arg	Leu	Lys	Gln	Pro	Pro	Ile	Ile	Val	Pro	Ile	Ile	Arg	Ala	Gly	Leu	
65					70					75					80	
Gly	Met	Ile	Asp	Pro	Ala	Leu	Ser	Met	Ile	Pro	Asp	Ala	Gln	Val	Gly	
				85					90					95		
Phe	Ile	Gly	Leu	Ala	Arg	Asp	Glu	Glu	Thr	His	Glu	Pro	Val	Pro	Tyr	
			100					105					110			
Leu	Glu	Ala	Leu	Pro	Gln	Asp	Leu	Ser	Asn	Gln	Pro	Val	Phe	Leu	Val	
		115					120					125				
Asp	Pro	Met	Leu	Ala	Thr	Gly	Gly	Ser	Leu	Leu	His	Ala	Ile	Arg	Leu	
	130					135					140					
Leu	Ala	Asp	Arg	Gly	Ala	Thr	Asp	Ile	Thr	Ala	Ile	Cys	Met	Val	Ser	
145					150					155					160	
Ala	Gln	Pro	Gly	Val	Asp	Ala	Leu	Ala	Glu	Ser						
				165					170							

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<400> 1109
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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
                                         Val Gly Val Leu Pro
                                         1                               5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
                        10                        15                        20

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gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
      25                      30                      35

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
      40                      45                      50

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
      55                      60                      65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
      70                      75                      80                      85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
      90                      95                      100

ggg gct cga atc gga cgc atc 424
Gly Ala Arg Ile Gly Arg Ile
      105

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<210> 1110  
 <211> 108  
 <212> PRT  
 <213> Corynebacterium glutamicum

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<400> 1110
Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg
  1                      5                      10                      15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
      20                      25                      30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
      35                      40                      45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
      50                      55                      60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
      65                      70                      75                      80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
      85                      90                      95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile
      100                      105

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<210> 1111  
 <211> 418  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(418)



&lt;223&gt; FRXA00450

&lt;400&gt; 1111

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gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115  
 Val Gly Val Leu Pro 5  
 1

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163  
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu 20  
 10 15

gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211  
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val 35  
 25 30

att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259  
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg 50  
 40 45

gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307  
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg 65  
 55 60

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355  
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr 85  
 70 75 80

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403  
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val 100  
 90 95

ggt gct cga atc gga 418  
 Gly Ala Arg Ile Gly 105

&lt;210&gt; 1112

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1112

Val Gly Val Leu Pro Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg  
 1 5 10 15

Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val  
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr  
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu  
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg  
 65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys  
 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly  
100 105

<210> 1113

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXA00465

<400> 1113

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tccccaacgc gcaccgaact tagccggatc gcagacttca cctggatgtc caccgcagcc 60
caagcgctac cagcgttgat gcgagggttg agcgcctaac atg act gaa gat gac 115
                                         Met Thr Glu Asp Asp
                                         1 5

tta gat ctg ctg cac cgc aca gta gaa cta gcc acc cag gca ctc aag 163
Leu Asp Leu Leu His Arg Thr Val Glu Leu Ala Thr Gln Ala Leu Lys
                        10 15 20

cag gga aac agt cct tat gga tcc ctg ctg gtt gat ccc ttc ggc gcg 211
Gln Gly Asn Ser Pro Tyr Gly Ser Leu Leu Val Asp Pro Phe Gly Ala
                        25 30 35

gtc gtt ttt gaa gac cac aac cga gat gcc gat ggg gat ctg acc aag 259
Val Val Phe Glu Asp His Asn Arg Asp Ala Asp Gly Asp Leu Thr Lys
                        40 45 50

cac ccg gaa ttc gcc atc gcc aaa tat gcg atc gaa aat tac agt gca 307
His Pro Glu Phe Ala Ile Ala Lys Tyr Ala Ile Glu Asn Tyr Ser Ala
                        55 60 65

tca gaa cgt gct gcg tgc act gtt tat acc tcg acg gaa cat tgc gcg 355
Ser Glu Arg Ala Ala Cys Thr Val Tyr Thr Ser Thr Glu His Cys Ala
                        70 75 80 85

atg tgc gcc ggt gcc cat gcg tgg gct gga ctg ggc aaa att tac tgc 403
Met Cys Ala Gly Ala His Ala Trp Ala Gly Leu Gly Lys Ile Tyr Cys
                        90 95 100

gcc acc aca ggt ggg caa aca gcc gct tgg tac gca aag tgg ggt gca 451
Ala Thr Thr Gly Gly Gln Thr Ala Ala Trp Tyr Ala Lys Trp Gly Ala
                        105 110 115

gaa tct ggg cct ttg aac ccg att tca gcg gac aaa att agc ccg aac 499
Glu Ser Gly Pro Leu Asn Pro Ile Ser Ala Asp Lys Ile Ser Pro Asn
                        120 125 130

ata tcc atc gaa gga cct gct tcc aga ttt gag gaa gtc ctg tat gaa 547
Ile Ser Ile Glu Gly Pro Ala Ser Arg Phe Glu Glu Val Leu Tyr Glu
                        135 140 145

ctg cat cga tgg ttt tat tta ggg cag tct ccg aat aag gct ctt 592
Leu His Arg Trp Phe Tyr Leu Gly Gln Ser Pro Asn Lys Ala Leu
150 155 160

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tagcgctggg catgtgactt taa

615

&lt;210&gt; 1114

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1114

Met	Thr	Glu	Asp	Asp	Leu	Asp	Leu	Leu	His	Arg	Thr	Val	Glu	Leu	Ala
1				5					10					15	

Thr	Gln	Ala	Leu	Lys	Gln	Gly	Asn	Ser	Pro	Tyr	Gly	Ser	Leu	Leu	Val
			20					25					30		

Asp	Pro	Phe	Gly	Ala	Val	Val	Phe	Glu	Asp	His	Asn	Arg	Asp	Ala	Asp
		35					40					45			

Gly	Asp	Leu	Thr	Lys	His	Pro	Glu	Phe	Ala	Ile	Ala	Lys	Tyr	Ala	Ile
	50					55					60				

Glu	Asn	Tyr	Ser	Ala	Ser	Glu	Arg	Ala	Ala	Cys	Thr	Val	Tyr	Thr	Ser
65					70					75					80

Thr	Glu	His	Cys	Ala	Met	Cys	Ala	Gly	Ala	His	Ala	Trp	Ala	Gly	Leu
				85					90					95	

Gly	Lys	Ile	Tyr	Cys	Ala	Thr	Thr	Gly	Gly	Gln	Thr	Ala	Ala	Trp	Tyr
			100					105					110		

Ala	Lys	Trp	Gly	Ala	Glu	Ser	Gly	Pro	Leu	Asn	Pro	Ile	Ser	Ala	Asp
		115					120					125			

Lys	Ile	Ser	Pro	Asn	Ile	Ser	Ile	Glu	Gly	Pro	Ala	Ser	Arg	Phe	Glu
130					135						140				

Glu	Val	Leu	Tyr	Glu	Leu	His	Arg	Trp	Phe	Tyr	Leu	Gly	Gln	Ser	Pro
145					150					155					160

Asn Lys Ala Leu

&lt;210&gt; 1115

&lt;211&gt; 1083

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1060)

&lt;223&gt; RXA00717

&lt;400&gt; 1115

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tcaatttcat	acgttttctc	tcaagattaa	ggacacttac	gtg	acc	cca	ccc	gct	115
				Val	Thr	Pro	Pro	Ala	
				1				5	

cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga	163
Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly	
10 15 20	
tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac	211
Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn	
25 30 35	
aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct	259
Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala	
40 45 50	
aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tcg atg	307
Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met	
55 60 65	
ggg ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtg	355
Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val	
70 75 80 85	
ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att	403
Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile	
90 95 100	
gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc	451
Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly	
105 110 115	
gtg cgc gtg gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc	499
Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg Val Asp Gly Val Arg	
120 125 130	
atc cac atc aac gag gac ctc gag tac ttc gtg ctc aac aag cct cgt	547
Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val Leu Asn Lys Pro Arg	
135 140 145	
ggc atg cac tcc acc atg agc gat gaa ctt ggt cgc cca tgc gtg ggt	595
Gly Met His Ser Thr Met Ser Asp Glu Leu Gly Arg Pro Cys Val Gly	
150 155 160 165	
gat ctg gtc agt gag aag act gca tct gga cag cgt ctg ttc cac gtc	643
Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln Arg Leu Phe His Val	
170 175 180	
ggg cgc ctc gac gcg gac acc gaa ggt ttg ctg ctg ctc acc aac gat	691
Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu Leu Leu Thr Asn Asp	
185 190 195	
ggg gag ttg gct aac cgc ctc atg cac cct aag tac gaa gtg tcc aag	739
Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys Tyr Glu Val Ser Lys	
200 205 210	
act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc	787
Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser	
215 220 225	
gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac	835
Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp	
230 235 240 245	
ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc	883

Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile  
 250 255 260

gaa atc cac gaa ggc cgc aag cac att gtg cga cgc ctc ttc gat gag 931  
 Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu  
 265 270 275

ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt 979  
 Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val  
 280 285 290

cag ctt ggt gat cag aag cca ggt tcc ctt cgt gca ctg aac tcc tct  
 1027

Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg Ala Leu Asn Ser Ser  
 295 300 305

gag ctg acc agc tta tac aag gtg gtc caa ctg tgacggaaat ttccaacatg  
 1080

Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu  
 310 315 320

cct  
 1083

<210> 1116  
 <211> 320  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 1116

Val Thr Pro Pro Ala Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser  
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Asn Arg Ser Gly Gly Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly  
 20 25 30

Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile  
 35 40 45

Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp  
 50 55 60

Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val  
 65 70 75 80

Arg Leu Gln Lys Val Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His  
 85 90 95

Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile  
 100 105 110

Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg  
 115 120 125

Val Asp Gly Val Arg Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val  
 130 135 140

Leu Asn Lys Pro Arg Gly Met His Ser Thr Met Ser Asp Glu Leu Gly  
 145 150 155 160

Arg Pro Cys Val Gly Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln  
 165 170 175  
 Arg Leu Phe His Val Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu  
 180 185 190  
 Leu Leu Thr Asn Asp Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys  
 195 200 205  
 Tyr Glu Val Ser Lys Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr  
 210 215 220  
 Asn Lys Leu Val Ser Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly  
 225 230 235 240  
 Pro Ala Lys Ala Asp Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys  
 245 250 255  
 Ser Leu Leu Arg Ile Glu Ile His Glu Gly Arg Lys His Ile Val Arg  
 260 265 270  
 Arg Leu Phe Asp Glu Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr  
 275 280 285  
 Lys Leu His Thr Val Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg  
 290 295 300  
 Ala Leu Asn Ser Ser Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu  
 305 310 315 320

&lt;210&gt; 1117

&lt;211&gt; 978

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(955)

&lt;223&gt; RXA01894

&lt;400&gt; 1117

agaatttttt cgaaaatgct ggcaccatca acagtgcacat tgtagaaac ttcaaggaga 60

acccatgaat gaaccggagc aacatcacgc gtccatgagg atg ccc aaa ccc aaa 115  
 Met Pro Lys Pro Lys  
 1 5

aat aat gcg ggt cga gat ctc aaa gct gcc att gct gtg ggg atc gga 163  
 Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile Ala Val Gly Ile Gly  
 10 15 20

ctg ggg gtc ctg gtt ctt ttg ggg att gtc cta agc cca tgg ggt tgg 211  
 Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu Ser Pro Trp Gly Trp  
 25 30 35

tac atc ctc gtt gca ggt ttt atg gct gca gca aca tgg gaa gtt ggt 259  
 Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val Gly

40	45	50	
agc aga ctt aaa gaa ggc ggc tat cat ttg cca ctg ccg att atg atc Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro Leu Pro Ile Met Ile 55 60 65			307
atc ggc ggt cag gca atc atc tgg ctg tca tgg cca ttt ggc acg atg Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp Pro Phe Gly Thr Met 70 75 80 85			355
ggc att ttg gcg tct ttt gtg gcc act gtg ttg gtg ctg atg tat ttc Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr Phe 90 95 100			403
cga att ttc tac aat ggc acg gaa aaa gaa gcc cgc aac tat ttg agg Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala Arg Asn Tyr Leu Arg 105 110 115			451
gac acc tct gtg ggc atc ttc gtg ctc acc tgg att cca ttg ttc gga Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe Gly 120 125 130			499
agc ttc gct gcg atg ctg tgc ctg atg caa aac aat tcc atc ccg ggt Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro Gly 135 140 145			547
aca tat ttc att ttg acg ttc atg ctg tgt gtg atc gca tgc gat gtg Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp Val 150 155 160 165			595
ggc ggg tat atc gcg ggt gtg ttc ttt gga tgc cac cca atg gcg ccg Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala Pro 170 175 180			643
ttg gtg agt ccg aag aag tct tgg gaa ggc ttt gcc ggc tcc att gtc Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile Val 185 190 195			691
tta gga tgc gtc act ggt gca ctc agt gtt cac ttc ctg ctc gat cac Leu Gly Ser Val Thr Gly Ala Leu Ser Val His Phe Leu Leu Asp His 200 205 210			739
cac tgg tgg atg ggt gtg atc ttg ggt tgt gcc cta gtt gtg tgc gcc His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys Ala 215 220 225			787
acg ttg ggt gac ttg gtt gag tgc cag ttc aaa cgc gat ttg ggc atc Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys Arg Asp Leu Gly Ile 230 235 240 245			835
aag gat atg tgc aac ctt ctt cca ggc cac ggc gga ttg atg gac cgt Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp Arg 250 255 260			883
ttg gat ggc atg ctc ccg gcc gcg atg gtg acg tgg ttg atc ctg agt Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr Trp Leu Ile Leu Ser 265 270 275			931
gtg atc agc agc tgc tat ccg tgc taaagcttgg gccagcttta agt Val Ile Ser Ser Ser Tyr Pro Ser 280 285			978

&lt;210&gt; 1118

&lt;211&gt; 285

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1118

Met Pro Lys Pro Lys Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile  
 1 5 10 15

Ala Val Gly Ile Gly Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu  
 20 25 30

Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala  
 35 40 45

Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro  
 50 55 60

Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp  
 65 70 75 80

Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu  
 85 90 95

Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala  
 100 105 110

Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp  
 115 120 125

Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn  
 130 135 140

Asn Ser Ile Pro Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val  
 145 150 155 160

Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser  
 165 170 175

His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe  
 180 185 190

Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His  
 195 200 205

Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala  
 210 215 220

Leu Val Val Cys Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys  
 225 230 235 240

Arg Asp Leu Gly Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly  
 245 250 255

Gly Leu Met Asp Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr  
 260 265 270

Trp Leu Ile Leu Ser Val Ile Ser Ser Ser Tyr Pro Ser  
 275 280 285





170										175					180					
ctg	gat	tcc	acc	tgc	tgg	atc	gta	gcg	tgt	ggg	caa	gcg	cga	ctt	cca	691				
Leu	Asp	Ser	Thr	Cys	Trp	Ile	Val	Ala	Cys	Gly	Gln	Ala	Arg	Leu	Pro					
			185					190					195							
gaa	gaa	tta	cgc	gat	gaa	cga	aaa	ggc	cct	acg	ggg	att	ggg	cat	tcc	739				
Glu	Glu	Leu	Arg	Asp	Glu	Arg	Lys	Gly	Pro	Thr	Gly	Ile	Gly	His	Ser					
		200					205					210								
atg	gtg	aca	aac	cca	cac	ggg	gaa	gta	att	gct	agc	gcg	ggg	tat	gag	787				
Met	Val	Thr	Asn	Pro	His	Gly	Glu	Val	Ile	Ala	Ser	Ala	Gly	Tyr	Glu					
		215				220					225									
cca	gaa	atg	ttg	atc	gcg	gat	att	gat	gtc	agc	ggg	ttg	gcc	aaa	att	835				
Pro	Glu	Met	Leu	Ile	Ala	Asp	Ile	Asp	Val	Ser	Gly	Leu	Ala	Lys	Ile					
230					235					240				245						
cgg	gag	gca	ttg	cct	gtt	ctt	taaccactgt	ctaaggaatc	act							879				
Arg	Glu	Ala	Leu	Pro	Val	Leu														
					250															

&lt;210&gt; 1120

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1120

Met	Asp	Asn	Phe	Ala	Leu	Leu	Arg	Asp	Ala	Ala	Glu	Lys	Ala	Ala	Glu
1				5					10					15	

Gln	Gly	Ala	Arg	Val	Leu	Val	Phe	Pro	Glu	Ala	Thr	Ser	Gln	Ser	Phe
			20					25					30		

Gly	Thr	Gly	Arg	Leu	Asp	Thr	Gln	Ala	Glu	Glu	Leu	Asp	Gly	Glu	Phe
		35					40					45			

Ser	Thr	Ala	Val	Arg	Lys	Leu	Ala	Asp	Glu	Leu	Asp	Val	Val	Ile	Val
	50					55					60				

Ala	Gly	Met	Phe	Thr	Pro	Ala	Asp	Thr	Val	Gln	Arg	Gly	Glu	Lys	Thr
65					70					75				80	

Ile	Ser	Arg	Val	Asn	Asn	Thr	Val	Leu	Ile	Ser	Gly	Ala	Gly	Leu	His
				85					90					95	

Gln	Gly	Tyr	Asn	Lys	Ile	His	Thr	Tyr	Asp	Ala	Phe	Gly	Tyr	Arg	Glu
			100					105					110		

Ser	Asp	Thr	Val	Lys	Pro	Gly	Asp	Glu	Leu	Val	Val	Phe	Glu	Val	Asp
		115					120					125			

Asp	Ile	Lys	Phe	Gly	Val	Ala	Thr	Cys	Tyr	Asp	Ile	Arg	Phe	Pro	Glu
	130					135					140				

Gln	Phe	Lys	Asp	Leu	Ala	Arg	Asn	Gly	Ala	Gln	Ile	Ile	Val	Val	Pro
145					150					155					160

Thr	Ser	Trp	Gln	Asp	Gly	Pro	Gly	Lys	Leu	Glu	Gln	Trp	Glu	Val	Leu
			165						170					175	

Pro	Arg	Ala	Arg	Ala	Leu	Asp	Ser	Thr	Cys	Trp	Ile	Val	Ala	Cys	Gly
			180					185					190		
Gln	Ala	Arg	Leu	Pro	Glu	Glu	Leu	Arg	Asp	Glu	Arg	Lys	Gly	Pro	Thr
		195					200					205			
Gly	Ile	Gly	His	Ser	Met	Val	Thr	Asn	Pro	His	Gly	Glu	Val	Ile	Ala
	210					215					220				
Ser	Ala	Gly	Tyr	Glu	Pro	Glu	Met	Leu	Ile	Ala	Asp	Ile	Asp	Val	Ser
225					230					235					240
Gly	Leu	Ala	Lys	Ile	Arg	Glu	Ala	Leu	Pro	Val	Leu				
				245					250						

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<210> 1121
<211> 1528
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101) .. (1528)
<223> RXN01209
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<400> 1121  
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ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115  
Met Cys Glu Arg Pro  
1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163  
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val  
10 15 20

ttg	ggt	ggc	ggg	cca	aaa	aaa	gta	gct	gga	att	gtt	gac	agc	gca	att	211
Leu	Gly	Gly	Gly	Pro	Lys	Lys	Val	Ala	Gly	Ile	Val	Asp	Ser	Ala	Ile	
			25					30					35			

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259  
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val  
40 45 50

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct 307  
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala  
55 60 65

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag 355  
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu  
70 75 80 85

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa 403  
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln  
90 95 100

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451  
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu  
105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt	499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
120 125 130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg	547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag	595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
150 155 160 165	
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga	643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
170 175 180	
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac	691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	
185 190 195	
ggc ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct	739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	
200 205 210	
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa	787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
215 220 225	
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat	835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
230 235 240 245	
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
250 255 260	
ggc ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac	979
Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His	
280 285 290	
ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag	
1027	
Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln	
295 300 305	
ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc	
1075	
Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly	
310 315 320 325	
atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt	
1123	
Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly	
330 335 340	

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
 1171  
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
                   345                                  350                                  355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
 1219  
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
                   360                                  365                                  370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
 1267  
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
                   375                                  380                                  385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
 1315  
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390                                  395                                  400                                  405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363  
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
                                   410                                  415                                  420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
 1411  
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
                                   425                                  430                                  435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
 1459  
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
                   440                                  445                                  450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
 1507  
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
                   455                                  460                                  465

gcc gcc ggc gaa agc gtg gaa  
 1528  
 Ala Ala Gly Glu Ser Val Glu  
 470                                  475

<210> 1122

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 1122

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
   1                                  5                                  10                                  15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
                   20                                  25                                  30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
                   35                                  40                                  45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
 50 55 60  
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
 65 70 75 80  
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
 85 90 95  
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
 100 105 110  
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
 115 120 125  
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
 130 135 140  
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
 145 150 155 160  
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
 165 170 175  
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
 180 185 190  
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
 195 200 205  
 Ala Asn Pro Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
 210 215 220  
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
 225 230 235 240  
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
 245 250 255  
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
 260 265 270  
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285  
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365  
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn

370	375	380
Ile Pro Glu Leu Ala Val	Leu Cys Asp Ser Ala	Pro Ala Ile Thr Met
385	390	395 400
Asp Glu Ala Ile	Ala Gln Ala Gln Gly Phe	Ala Arg Thr His Asp Thr
	405	410 415
Ile Val Ile	Val Lys Gly Gly His Leu Thr	Gly Ala Leu Ala Asp Asn
	420	425 430
Ala Val Val	Arg Pro Asp Gly Ser Val Phe Gln	Val Glu Asn Leu Arg
	435	440 445
Val Asn Thr	Thr Asn Ser His Gly Thr Gly Cys	Ser Leu Ser Ala Ser
	450	455 460
Leu Ala Thr	Lys Ile Ala Ala Gly Glu Ser	Val Glu
465	470	475

&lt;210&gt; 1123

&lt;211&gt; 1528

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)...(1528)

&lt;223&gt; FRXA01209

&lt;400&gt; 1123

cagattgcag cacagaaggc atcggcgcca ggcagctttg cggtggcggtt tattgatgcg 60

ctttatgacg tggatgccca ggctgtggcc tcgttggttg	atg tgc gag agg cct	115
	Met Cys Glu Arg Pro	
	1 5	

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt	163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val	
10 15 20	

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att	211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile	
25 30 35	

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg	259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	
40 45 50	

gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct	307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	
55 60 65	

cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag	355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	
70 75 80 85	

ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa	403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	
90 95 100	

gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa 451  
 Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu  
 105 110 115

aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt 499  
 Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly  
 120 125 130

gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg 547  
 Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala  
 135 140 145

acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag 595  
 Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu  
 150 155 160 165

atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga 643  
 Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly  
 170 175 180

ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac 691  
 Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp  
 185 190 195

ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct 739  
 Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala  
 200 205 210

gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa 787  
 Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu  
 215 220 225

act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat 835  
 Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn  
 230 235 240 245

tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca 883  
 Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr  
 250 255 260

ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc 931  
 Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly  
 265 270 275

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979  
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His  
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
 1027  
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
 1075  
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
 1123



Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
1507

Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
455 460 465

gcc gcc ggc gaa agc gtg gaa  
1528

Ala Ala Gly Glu Ser Val Glu  
470 475

<210> 1124

<211> 476

<212> PRT

<213> *Corynebacterium glutamicum*

**<400> 1124**

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
1 5 10 15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
 35 40 45  
 Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
 50 55 60  
 Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
 65 70 75 80  
 Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
 85 90 95  
 Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
 100 105 110  
 Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
 115 120 125  
 Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
 130 135 140  
 Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
 145 150 155 160  
 Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
 165 170 175  
 Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
 180 185 190  
 Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
 195 200 205  
 Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
 210 215 220  
 Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
 225 230 235 240  
 Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
 245 250 255  
 Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
 260 265 270  
 Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285  
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300  
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320  
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335  
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu

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          355              360              365
Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370              375              380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
385              390              395              400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
              405              410              415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
              420              425              430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
              435              440              445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
              450              455              460

Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
465              470              475

<210> 1125
<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> RXN01617

<400> 1125
tcagaagcta ccggcggcgc cggcatccag gttgattga agaccttcca gcatttaaga 60

tgtttatggc attgggtcca tcacatgctt ggggtggcctt ttg atc cta aag aca 115
              Leu Ile Leu Lys Thr
              1              5

act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat 163
Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn
              10              15              20

cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc 211
Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile
              25              30              35

ggg atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg 259
Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu
              40              45              50

gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc 307
Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys
              55              60              65

aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc 355
Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg
              70              75              80              85

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gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag 403  
 Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu  
                     90                                    95                                    100

gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg 451  
 Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu  
                     105                                    110                                    115

aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt 499  
 Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val  
                     120                                    125                                    130

gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt 547  
 Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu  
                     135                                    140                                    145

ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac 595  
 Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp  
                     150                                    155                                    160                                    165

gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca 643  
 Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala  
                     170                                    175                                    180

gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag 691  
 Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys  
                     185                                    190                                    195

cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg 739  
 Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro  
                     200                                    205                                    210

ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc 792  
 Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
                     215                                    220

cct 795

<210> 1126

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 1126

Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala  
                     1                                    5                                    10                                    15

Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu  
                     20                                    25                                    30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr  
                     35                                    40                                    45

Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp  
                     50                                    55                                    60

Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr  
                     65                                    70                                    75                                    80

Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr

85								90				95			
Pro	Asn	Asn	Phe	Glu	Ala	Thr	Thr	Leu	Ser	Gly	Leu	Asp	Lys	Leu	Glu
			100					105					110		
Thr	Ile	Asp	Asp	Leu	Lys	Glu	Ala	Ala	Arg	Leu	Ile	His	Glu	Gln	Gly
		115					120					125			
Pro	Gln	Tyr	Val	Val	Val	Lys	Gly	Gly	Ile	Asp	Phe	Pro	Gly	Asp	Asn
	130					135					140				
Ala	Val	Asp	Val	Leu	Phe	Asp	Gly	Thr	Asp	Tyr	His	Val	Phe	Ser	Glu
145					150					155					160
Pro	Lys	Ile	Gly	Asp	Glu	Arg	Val	Ser	Gly	Ala	Gly	Cys	Thr	Phe	Ala
				165					170					175	
Ala	Val	Ile	Thr	Ala	Glu	Leu	Ala	Lys	Gly	Asn	Ser	Ala	Val	Asp	Ala
			180					185					190		
Val	Thr	Thr	Ala	Lys	Arg	Val	Val	Thr	Arg	Ala	Val	Lys	Asp	Ala	Val
		195					200					205			
Ala	Ser	Asn	Ala	Pro	Phe	Thr	Ser	Val	Trp	Leu	Ala	Glu	Asp	Asn	Lys
	210					215					220				

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<210> 1127
<211> 638
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1)..(615)  
<223> FRXA01617
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<400> 1127																
gct	aat	cag	att	gag	gcc	gcc	acc	gca	gcg	cac	gat	ctt	gat	gtg	gtg	48
Ala	Asn	Gln	Ile	Glu	Ala	Ala	Thr	Ala	Ala	His	Asp	Leu	Asp	Val	Val	
1				5					10					15		
aag	atc	ggt	atg	ttg	ggt	act	cct	gca	acg	atc	gat	act	gtg	gca	acc	96
Lys	Ile	Gly	Met	Leu	Gly	Thr	Pro	Ala	Thr	Ile	Asp	Thr	Val	Ala	Thr	
			20					25					30			
gct	ttg	gag	gaa	aac	agc	ttc	aag	cac	gtt	gtc	cta	gac	ccg	gta	ctg	144
Ala	Leu	Glu	Glu	Asn	Ser	Phe	Lys	His	Val	Val	Leu	Asp	Pro	Val	Leu	
		35					40					45				
atc	tgc	aag	ggc	cag	gag	ccc	ggc	gcg	gca	ctt	gat	act	gac	act	gcc	192
Ile	Cys	Lys	Gly	Gln	Glu	Pro	Gly	Ala	Ala	Leu	Asp	Thr	Asp	Thr	Ala	
	50					55					60					
ctt	cgc	gcg	aag	gtg	ctg	cca	cag	gca	acc	gtg	ggt	act	cca	aac	aac	240
Leu	Arg	Ala	Lys	Val	Leu	Pro	Gln	Ala	Thr	Val	Val	Thr	Pro	Asn	Asn	
65				70						75				80		

```

ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac 288
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
      85                      90                      95

gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac 336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
      100                      105                      110

gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac 384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp
      115                      120                      125

gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc 432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile
      130                      135                      140

ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc 480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile
      145                      150                      155                      160

acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc 528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr
      165                      170                      175

gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac 576
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn
      180                      185                      190

gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt 625
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
      195                      200                      205

aaacaagctc cct 638

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&lt;210&gt; 1128

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1128

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Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
  1              5              10              15

Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
      20              25              30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
      35              40              45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala
      50              55              60

Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn
      65              70              75              80

Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp
      85              90              95

Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr
      100              105              110

```

Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp  
 115 120 125

Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile  
 130 135 140

Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile  
 145 150 155 160

Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr  
 165 170 175

Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn  
 180 185 190

Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
 195 200 205

&lt;210&gt; 1129

&lt;211&gt; 792

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(769)

&lt;223&gt; RXC01600

&lt;400&gt; 1129

tgagtacaaa tctcgtccaa cccatgctca tccactgttt tacggcctgg tgaagaccgc 60

tttgagactg cgtgtccacc cttagatcta caatgtgatc atg gtt tcg aag atg 115  
 Met Val Ser Lys Met  
 1 5

cac att ccc ggt acc cat gag ttc acg gtg aca gat act gaa ctg ttg 163  
 His Ile Pro Gly Thr His Glu Phe Thr Val Thr Asp Thr Glu Leu Leu  
 10 15 20

tta gag tcc cca att ttg ggc gtt cgt cga gat tca ttg atc atg ccg 211  
 Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp Ser Leu Ile Met Pro  
 25 30 35

ggt ggt tcc act gcc cgc cgt gaa gtg gtt gaa cac ttt ggg gcg gtc 259  
 Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu His Phe Gly Ala Val  
 40 45 50

gca gtg gtt gcc ttt gat ggt gaa aac att gcg atg gtc aag cag tac 307  
 Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala Met Val Lys Gln Tyr  
 55 60 65

cgt cgc agc gtg ggg gat tcc ttg tgg gag ctg cct gca ggt ttg ttg 355  
 Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu Pro Ala Gly Leu Leu  
 70 75 80 85

gat att gct gat gag gat gaa ctc acg ggc gcg cag cgc gag ctc atg 403  
 Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala Gln Arg Glu Leu Met  
 90 95 100

gag gag gct ggt ttg gag gcc agt gag tgg tcc gtg ctc act gat ttg 451  
 Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser Val Leu Thr Asp Leu  
 105 110 115  
 att acc tcg cct ggt ttc tgc gat gaa gcg gtg cgt gtc ttt cta gcc 499  
 Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val Arg Val Phe Leu Ala  
 120 125 130  
 cga ggc ctc aca aag gtt gag cgc ccg aag gtt atg ggc gat gaa gaa 547  
 Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val Met Gly Asp Glu Glu  
 135 140 145  
 gcg gac atg att aac cag tgg gtt ccg cta cat gag gca gtg gga atg 595  
 Ala Asp Met Ile Asn Gln Trp Val Pro Leu His Glu Ala Val Gly Met  
 150 155 160 165  
 gtg ttt agt ggc cag ttg gtt aac tcc att gcc att gcg ggt gtc atg 643  
 Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala Ile Ala Gly Val Met  
 170 175 180  
 gct gct gat gct gtg att gcg ggt cgt gcg tct gcg cgt gcc gtc acc 691  
 Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser Ala Arg Ala Val Thr  
 185 190 195  
 gcg ccg ttt acc tat cgc cct acg gcg ttg gcg cag cgt cga aaa gcg 739  
 Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala Gln Arg Arg Lys Ala  
 200 205 210  
 cac ggc att gtt cct gac atg aaa aaa cta tgaaggctcg cgtttttagcg 789  
 His Gly Ile Val Pro Asp Met Lys Lys Leu  
 215 220  
 aaa 792

&lt;210&gt; 1130

&lt;211&gt; 223

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1130

Met Val Ser Lys Met His Ile Pro Gly Thr His Glu Phe Thr Val Thr  
 1 5 10 15  
 Asp Thr Glu Leu Leu Leu Glu Ser Pro Ile Leu Gly Val Arg Arg Asp  
 20 25 30  
 Ser Leu Ile Met Pro Gly Gly Ser Thr Ala Arg Arg Glu Val Val Glu  
 35 40 45  
 His Phe Gly Ala Val Ala Val Val Ala Phe Asp Gly Glu Asn Ile Ala  
 50 55 60  
 Met Val Lys Gln Tyr Arg Arg Ser Val Gly Asp Ser Leu Trp Glu Leu  
 65 70 75 80  
 Pro Ala Gly Leu Leu Asp Ile Ala Asp Glu Asp Glu Leu Thr Gly Ala  
 85 90 95  
 Gln Arg Glu Leu Met Glu Glu Ala Gly Leu Glu Ala Ser Glu Trp Ser  
 100 105 110



Val Leu Thr Asp Leu Ile Thr Ser Pro Gly Phe Cys Asp Glu Ala Val  
 115 120 125

Arg Val Phe Leu Ala Arg Gly Leu Thr Lys Val Glu Arg Pro Lys Val  
 130 135 140

Met Gly Asp Glu Glu Ala Asp Met Ile Asn Gln Trp Val Pro Leu His  
 145 150 155 160

Glu Ala Val Gly Met Val Phe Ser Gly Gln Leu Val Asn Ser Ile Ala  
 165 170 175

Ile Ala Gly Val Met Ala Ala Asp Ala Val Ile Ala Gly Arg Ala Ser  
 180 185 190

Ala Arg Ala Val Thr Ala Pro Phe Thr Tyr Arg Pro Thr Ala Leu Ala  
 195 200 205

Gln Arg Arg Lys Ala His Gly Ile Val Pro Asp Met Lys Lys Leu  
 210 215 220

&lt;210&gt; 1131

&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(703)

&lt;223&gt; RXC01622

&lt;400&gt; 1131

aaggcgtggg cgtttttgaa ggagcttcgt ttggagcgcg gtcctttgga tcgtgaagtt 60

gccatcgag agctgaagag ctggtgggaa ggagaaaaca\*atg agt gat ttt tat 115  
 Met Ser Asp Phe Tyr  
 1 5

gcc gac agg ttg ttt aac gcg atg gag cgc aat gag gta gct cca ggc 163  
 Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn Glu Val Ala Pro Gly  
 10 15 20

atg ttg ttg gtg gct gcg ccc gat atg gcg tcg gag gat ttt gag cgc 211  
 Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser Glu Asp Phe Glu Arg  
 25 30 35

agc atc gtg ttg atc atc gag cat tct cct gcc acc act ttt ggt gtg 259  
 Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala Thr Thr Phe Gly Val  
 40 45 50

aac att tct tca cgt tcc gat gtt gct gtg gcc aat gtg ttg ccc gag 307  
 Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala Asn Val Leu Pro Glu  
 55 60 65

tgg gtg gac ctc acc tcg aag cca cag gca ctg tac atc ggt ggg ccg 355  
 Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu Tyr Ile Gly Gly Pro  
 70 75 80 85

ttg agc cag cag gct gtg gtt ggt ttg ggc gtg acc aag ccg ggc gtg 403

Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val Thr Lys Pro Gly Val  
                             90                            95                            100  
 gat att gaa aat tcc acc agc ttc aac aag ctc gcc aac cgc ctg gtg 451  
 Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu Ala Asn Arg Leu Val  
                             105                            110                            115  
 cac gtg gat ctg cgt tct gca cct gaa gat gtg gct gat gat ctt gag 499  
 His Val Asp Leu Arg Ser Ala Pro Glu Asp Val Ala Asp Asp Leu Glu  
                             120                            125                            130  
 ggc atg cgc ttt ttt gcg ggc tac gcg gag tgg gct ccg ggc cag ctc 547  
 Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp Ala Pro Gly Gln Leu  
                             135                            140                            145  
 aac gag gaa att gag cag ggt gat tgg ttc gtc aca cct gcg ttg ccg 595  
 Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val Thr Pro Ala Leu Pro  
                             150                            155                            160                            165  
 tcg gac att atc gcg ccg ggc cgc gtc gat att tgg ggc gac gtg atg 643  
 Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile Trp Gly Asp Val Met  
                             170                            175                            180  
 cgt cga caa gca atg cct ttg ccg ttg tat tcc acg ttt ccg tcg gac 691  
 Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser Thr Phe Pro Ser Asp  
                             185                            190                            195  
 cct tca gat aat tagatgagtt ccgaaaattt aaa 726  
 Pro Ser Asp Asn  
                             200

&lt;210&gt; 1132

&lt;211&gt; 201

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1132

Met Ser Asp Phe Tyr Ala Asp Arg Leu Phe Asn Ala Met Glu Arg Asn  
   1                            5                            10                            15  
 Glu Val Ala Pro Gly Met Leu Leu Val Ala Ala Pro Asp Met Ala Ser  
                             20                            25                            30  
 Glu Asp Phe Glu Arg Ser Ile Val Leu Ile Ile Glu His Ser Pro Ala  
                             35                            40                            45  
 Thr Thr Phe Gly Val Asn Ile Ser Ser Arg Ser Asp Val Ala Val Ala  
                             50                            55                            60  
 Asn Val Leu Pro Glu Trp Val Asp Leu Thr Ser Lys Pro Gln Ala Leu  
                             65                            70                            75                            80  
 Tyr Ile Gly Gly Pro Leu Ser Gln Gln Ala Val Val Gly Leu Gly Val  
                             85                            90                            95  
 Thr Lys Pro Gly Val Asp Ile Glu Asn Ser Thr Ser Phe Asn Lys Leu  
                             100                            105                            110  
 Ala Asn Arg Leu Val His Val Asp Leu Arg Ser Ala Pro Glu Asp Val  
                             115                            120                            125

Ala Asp Asp Leu Glu Gly Met Arg Phe Phe Ala Gly Tyr Ala Glu Trp  
 130 135 140

Ala Pro Gly Gln Leu Asn Glu Glu Ile Glu Gln Gly Asp Trp Phe Val  
 145 150 155 160

Thr Pro Ala Leu Pro Ser Asp Ile Ile Ala Pro Gly Arg Val Asp Ile  
 165 170 175

Trp Gly Asp Val Met Arg Arg Gln Ala Met Pro Leu Pro Leu Tyr Ser  
 180 185 190

Thr Phe Pro Ser Asp Pro Ser Asp Asn  
 195 200

&lt;210&gt; 1133

&lt;211&gt; 1827

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1804)

&lt;223&gt; RXC00128

&lt;400&gt; 1133

ccattttccg tttggtcttg cctaaagaac cgcattggaaa ttatcgtgaa gcaccgatcc 60

cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115  
 Val Ser Lys Ile Ser  
 1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163  
 Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val  
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gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211  
 Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg  
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tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259  
 Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro  
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 Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala  
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tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355  
 Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly  
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 Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg  
 90 95 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451  
 Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile  
 105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat	499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr	
120 125 130	
cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa	547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu	
135 140 145	
gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag	595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu	
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Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe	
170 175 180	
gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat	691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	
185 190 195	
gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt	739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly	
200 205 210	
cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat	787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp	
215 220 225	
gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg	835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu	
230 235 240 245	
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg	883
Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val	
250 255 260	
tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct	931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala	
265 270 275	
gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac	979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp	
280 285 290	
ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg	
1027	
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu	
295 300 305	
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1075	
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val	
310 315 320 325	
agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg	
1123	
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala	
330 335 340	

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac  
1171  
Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn  
345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg  
1219  
Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala  
360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt  
1267  
Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser  
375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga  
1315  
Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg  
390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg  
1363  
Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu  
410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act  
1411  
Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr  
425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc  
1459  
Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val  
440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag  
1507  
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu  
455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca  
1555  
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro  
470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg  
1603  
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp  
490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat  
1651  
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn  
505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac  
1699  
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr  
520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat  
1747

Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp  
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg  
1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val  
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gtt gcg tac tgatggagct gttcttcccg cgc  
1827

Val Ala Tyr

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<211> 568

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1134

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser  
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Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp  
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile  
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe  
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala  
65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr  
85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn  
100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu  
115 120 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile  
130 135 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp  
145 150 155 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His  
165 170 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg  
180 185 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala  
195 200 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn  
 210 215 220  
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr  
 225 230 235 240  
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Ala Arg Leu Arg Phe  
 245 250 255  
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro  
 260 265 270  
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr  
 275 280 285  
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn  
 290 295 300  
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val  
 305 310 315 320  
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp  
 325 330 335  
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val  
 340 345 350  
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly  
 355 360 365  
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe  
 370 375 380  
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro  
 385 390 395 400  
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu  
 405 410 415  
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe  
 420 425 430  
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys  
 435 440 445  
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val  
 450 455 460  
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser  
 465 470 475 480  
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro  
 485 490 495  
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser  
 500 505 510  
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser  
 515 520 525  
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro

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Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
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Arg Ala Ala Pro Val Val Ala Tyr
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<213> Corynebacterium glutamicum

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<222> (101)..(532)
<223> RXC01709

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gaaattaggt gtcgatgcag caatacggaa ctttgccaat gtg ttt gaa caa gct 115
              Val Phe Glu Gln Ala
              1              5

ctc ggg ctc acc acc ctt gca caa aca gct gga gcg ggc gca gcg ggg 163
Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly Ala Gly Ala Ala Gly
              10              15              20

ggc ttg ggt ttc atg gca atg gcg ttg ttg tct gca ggg atg cgc tcc 211
Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser Ala Gly Met Arg Ser
              25              30              35

ggc gtg gac atg att ctt aat gaa acc ggg ggt gaa aag atg ctt gca 259
Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys Met Leu Ala
              40              45              50

cag gca gat tta gtc atc act gga gaa gga cgc att gat gca cag acc 307
Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp Ala Gln Thr
              55              60              65

ctc agc ggg aaa gct cct act gga atc gcc aaa cgg gca cgt gcg aaa 355
Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala Arg Ala Lys
              70              75              80              85

gga att cca gta ctg gcg gtt tgt ggg cag agc cta ttg ggt cca gca 403
Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu Gly Pro Ala
              90              95              100

atc tca aat gag cta ttt gaa gac atc tac agc ttt acc gat ttc gaa 451
Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr Asp Phe Glu
              105              110              115

tct gac atc aat gaa tgc att cga aac ccg ctc cca att ttg gaa ggt 499
Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile Leu Glu Gly
              120              125              130

atc ggt ttt aac atc gcc aaa cat cat ctg agt tagcgatatt tcagcaaacc 552
Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
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gat

555

&lt;210&gt; 1136

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1136

Val Phe Glu Gln Ala Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly  
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Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser  
 20 25 30

Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly  
 35 40 45

Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg  
 50 55 60

Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys  
 65 70 75 80

Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser  
 85 90 95

Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser  
 100 105 110

Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu  
 115 120 125

Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser  
 130 135 140

&lt;210&gt; 1137

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(898)

&lt;223&gt; RXC02207

&lt;400&gt; 1137

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gggtccaatta cattcactgg taatctgaaa ccttgtgaat atg cgc cgt cga tcc 115  
 Met Arg Arg Arg Ser  
 1 5

cgt gtg tcc cgt ttg ctt ccc gcc aca gct ttg ctg gcc tca act gca 163  
 Arg Val Ser Arg Leu Leu Pro Ala Thr Ala Leu Leu Ala Ser Thr Ala  
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ctt	ctt	tta	agt	gca	tgt	acg	caa	ggg	gta	acg	gac	tcc	ccg	gat	atg	211
Leu	Leu	Leu	Ser	Ala	Cys	Thr	Gln	Gly	Val	Thr	Asp	Ser	Pro	Asp	Met	
			25					30					35			
ggc	aag	gca	act	ccc	gct	gtc	tcc	ccc	gca	gca	agc	aac	ccg	gat	ggc	259
Gly	Lys	Ala	Thr	Pro	Ala	Val	Ser	Pro	Ala	Ala	Ser	Asn	Pro	Asp	Gly	
		40					45					50				
caa	gta	att	gag	ttc	ggc	aac	atc	act	gac	atg	gaa	gtc	act	gat	ggc	307
Gln	Val	Ile	Glu	Phe	Gly	Asn	Ile	Thr	Asp	Met	Glu	Val	Thr	Asp	Gly	
	55					60					65					
gac	atc	ctc	ggc	gta	cgc	acc	gaa	gac	gca	ctc	gct	att	ggc	aca	gtc	355
Asp	Ile	Leu	Gly	Val	Arg	Thr	Glu	Asp	Ala	Leu	Ala	Ile	Gly	Thr	Val	
70					75				80						85	
tcc	gac	ttc	gaa	gcg	ggc	agc	cag	gtg	gaa	ctg	gac	gtc	gat	aag	caa	403
Ser	Asp	Phe	Glu	Ala	Gly	Ser	Gln	Val	Glu	Leu	Asp	Val	Asp	Lys	Gln	
			90					95						100		
tgc	ggc	gac	ctg	acc	gca	acc	ggc	ggc	act	ttc	gtg	ctc	ccc	tgc	gcc	451
Cys	Gly	Asp	Leu	Thr	Ala	Thr	Gly	Gly	Thr	Phe	Val	Leu	Pro	Cys	Ala	
			105				110						115			
gat	ggc	gtt	tat	ttg	att	gat	gcc	aag	gac	ccg	gat	ctg	gat	gag	ttg	499
Asp	Gly	Val	Tyr	Leu	Ile	Asp	Ala	Lys	Asp	Pro	Asp	Leu	Asp	Glu	Leu	
		120					125					130				
cgt	gca	act	gac	aag	cca	gtc	acg	gtg	gca	gcc	ttg	acc	agc	gat	gat	547
Arg	Ala	Thr	Asp	Lys	Pro	Val	Thr	Val	Ala	Ala	Leu	Thr	Ser	Asp	Asp	
	135					140					145					
cag	ctt	ctg	gtg	ggc	aat	ggc	gaa	gat	gaa	gaa	ctc	acc	atc	tac	cgc	595
Gln	Leu	Leu	Val	Gly	Asn	Gly	Glu	Asp	Glu	Glu	Leu	Thr	Ile	Tyr	Arg	
150					155					160					165	
gag	ggc	gaa	gag	cca	gaa	acc	ttc	acc	gtc	gcg	ggc	ccc	aat	acc	cag	643
Glu	Gly	Glu	Glu	Pro	Glu	Thr	Phe	Thr	Val	Ala	Gly	Pro	Asn	Thr	Gln	
				170					175					180		
ctc	atc	gcc	gtt	cct	gtc	att	gat	cgc	cac	gac	gcc	gtt	gtg	cgc	acc	691
Leu	Ile	Ala	Val	Pro	Val	Ile	Asp	Arg	His	Asp	Ala	Val	Val	Arg	Thr	
			185					190					195			
tgg	aac	gaa	aac	acc	acg	att	caa	gat	gtg	gac	tac	ccc	aac	gac	cgt	739
Trp	Asn	Glu	Asn	Thr	Thr	Ile	Gln	Asp	Val	Asp	Tyr	Pro	Asn	Asp	Arg	
		200					205					210				
gaa	ggc	gcg	acc	ctt	cgc	gtg	gga	ctc	ggc	gtt	ggc	caa	atg	gct	ggc	787
Glu	Gly	Ala	Thr	Leu	Arg	Val	Gly	Leu	Gly	Val	Gly	Gln	Met	Ala	Gly	
	215					220					225					
ggc	gaa	gac	ggc	ctg	ctg	gtg	gtc	tct	gat	gaa	atg	ggc	ggc	caa	att	835
Gly	Glu	Asp	Gly	Leu	Leu	Val	Val	Ser	Asp	Glu	Met	Gly	Gly	Gln	Ile	
230					235					240					245	
gcc	atc	tac	aac	gct	gat	gat	gtc	atc	cga	ctt	caa	aac	gac	cgc	ccc	883
Ala	Ile	Tyr	Asn	Ala	Asp	Asp	Val	Ile	Arg	Leu	Gln	Asn	Asp	Arg	Pro	
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cac cga cga gga acc  
His Arg Arg Gly Thr  
265

898

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<211> 266  
<212> PRT  
<213> Corynebacterium glutamicum

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Asp Ser Pro Asp Met Gly Lys Ala Thr Pro Ala Val Ser Pro Ala Ala  
35 40 45  
Ser Asn Pro Asp Gly Gln Val Ile Glu Phe Gly Asn Ile Thr Asp Met  
50 55 60  
Glu Val Thr Asp Gly Asp Ile Leu Gly Val Arg Thr Glu Asp Ala Leu  
65 70 75 80  
Ala Ile Gly Thr Val Ser Asp Phe Glu Ala Gly Ser Gln Val Glu Leu  
85 90 95  
Asp Val Asp Lys Gln Cys Gly Asp Leu Thr Ala Thr Gly Gly Thr Phe  
100 105 110  
Val Leu Pro Cys Ala Asp Gly Val Tyr Leu Ile Asp Ala Lys Asp Pro  
115 120 125  
Asp Leu Asp Glu Leu Arg Ala Thr Asp Lys Pro Val Thr Val Ala Ala  
130 135 140  
Leu Thr Ser Asp Asp Gln Leu Leu Val Gly Asn Gly Glu Asp Glu Glu  
145 150 155 160  
Leu Thr Ile Tyr Arg Glu Gly Glu Glu Pro Glu Thr Phe Thr Val Ala  
165 170 175  
Gly Pro Asn Thr Gln Leu Ile Ala Val Pro Val Ile Asp Arg His Asp  
180 185 190  
Ala Val Val Arg Thr Trp Asn Glu Asn Thr Thr Ile Gln Asp Val Asp  
195 200 205  
Tyr Pro Asn Asp Arg Glu Gly Ala Thr Leu Arg Val Gly Leu Gly Val  
210 215 220  
Gly Gln Met Ala Gly Gly Glu Asp Gly Leu Leu Val Val Ser Asp Glu  
225 230 235 240  
Met Gly Gly Gln Ile Ala Ile Tyr Asn Ala Asp Asp Val Ile Arg Leu  
245 250 255  
Gln Asn Asp Arg Pro His Arg Arg Gly Thr  
260 265

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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(868)  
<223> RXA00347
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Met Thr Leu Thr Ile  
1 5

gag gaa atc gcc aag acc aaa aag ctt ttg gtt gtg tcc gat ttt gat 163  
Glu Glu Ile Ala Lys Thr Lys Lys Leu Leu Val Val Ser Asp Phe Asp  
10 15 20

gga acc atc gca gga ttt agc aag gac gct tac aac gtt cct atc aac 211  
Gly Thr Ile Ala Gly Phe Ser Lys Asp Ala Tyr Asn Val Pro Ile Asn  
25 30 35

cag aaa tcc ctc aag gcg gta aaa gac ctc tcc caa caa gca gac act 259  
Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser Gln Gln Ala Asp Thr  
40 45 50

gat gtt gtc att ttg tcg gga cgt cac ctg gag gga ttg aag acg gtt 307  
Asp Val Val Ile Leu Ser Gly Arg His Leu Glu Gly Leu Lys Thr Val  
55 60 65

ctt gat ctt ggt cag tac gac atc acc atg gtg ggt tca cac ggt tct 355  
Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val Gly Ser His Gly Ser  
70 75 80 85

gag gat tcc tcc cgc ccg cgt acc ctc act cct gaa gag gta gct cgc 403  
Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro Glu Glu Val Ala Arg  
90 95 100

ctc gcc aag att gaa gca gat ctg gaa aag atc gtc gac ggc atc gaa 451  
Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile Val Asp Gly Ile Glu  
105 110 115

ggc gca ttc gtg gag atc aag cct ttc cac cgc gtg ctg cac ttc atc 499  
Gly Ala Phe Val Glu Ile Lys Pro Phe His Arg Val Leu His Phe Ile  
120 125 130

cgt gtt tcc gac aag gac aaa gtc caa gga atc ctc gcc caa gca gca 547  
Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile Leu Ala Gln Ala Ala  
135 140 145

cac gta gac tct tcc ggc ctg aag gtt act aac ggc aag agc atc atc 595  
 His Val Asp Ser Ser Gly Leu Lys Val Thr Asn Gly Lys Ser Ile Ile  
 150 155 160 165

gaa tac tcc atc agc tcc acc acc aag ggc acc tgg ctg aag gaa tac 643  
Glu Tyr Ser Ile Ser Ser Thr Thr Lys Gly Thr Trp Leu Lys Glu Tyr

170	175	180	
gtt gac cgc acc gag ccc act ggt gtg att ttc ctc ggc gat gac acc			691
Val Asp Arg Thr Glu Pro Thr Gly Val Ile Phe Leu Gly Asp Asp Thr			
185	190	195	
acc gat gag cac ggt ttc aaa gct tta gaa aac gat gat cgt gcc cta			739
Thr Asp Glu His Gly Phe Lys Ala Leu Glu Asn Asp Asp Arg Ala Leu			
200	205	210	
acc gtc aag gtt ggc gaa gga gac act gca gcc aaa acc cgc gtc gac			787
Thr Val Lys Val Gly Glu Gly Asp Thr Ala Ala Lys Thr Arg Val Asp			
215	220	225	
gat gtt gat aat gtg gga att ttc cta gag aaa ctc gcc tac cac cgc			835
Asp Val Asp Asn Val Gly Ile Phe Leu Glu Lys Leu Ala Tyr His Arg			
230	235	240	245
atg cag tat gcg gaa agc gtg cga ttg ggg att taagagagcc taaacgcacg			888
Met Gln Tyr Ala Glu Ser Val Arg Leu Gly Ile			
250	255		
aaa			891
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Asn Val Pro Ile Asn Gln Lys Ser Leu Lys Ala Val Lys Asp Leu Ser			
35	40	45	
Gln Gln Ala Asp Thr Asp Val Val Ile Leu Ser Gly Arg His Leu Glu			
50	55	60	
Gly Leu Lys Thr Val Leu Asp Leu Gly Gln Tyr Asp Ile Thr Met Val			
65	70	75	80
Gly Ser His Gly Ser Glu Asp Ser Ser Arg Pro Arg Thr Leu Thr Pro			
85	90	95	
Glu Glu Val Ala Arg Leu Ala Lys Ile Glu Ala Asp Leu Glu Lys Ile			
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Val Leu His Phe Ile Arg Val Ser Asp Lys Asp Lys Val Gln Gly Ile			
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gcc cgc gcc atg cgc cgc gat aac ttc tcc acc gca ggc acc aac gtc  
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360 365 370

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1267  
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375 380 385

ccc gtc tac cgc gcc gac tac atc tcc ctc tca cgc acc acc gcc acc  
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Pro Val Tyr Arg Ala Asp Tyr Ile Ser Leu Ser Arg Thr Thr Ala Thr  
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gtc atc gcg gag atg tcc aaa cgc ttc ccc tcc cgg cgt gac gca ctc  
1363  
Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser Arg Arg Asp Ala Leu  
410 415 420

gac ctc atc gcg gcc gcc cta ctt ggc aat ggc gag gcc aaa atc cgc  
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425 430 435

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Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys Gly Val Glu Asp Thr  
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gcg ccg ggg aga ttc ggc gtc tcc gct gca gaa ttc cac ttg ctg cag  
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Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu Phe His Leu Leu Gln  
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gaa gaa cgc agc ctg ctg tgg cca cgc acc atg acc acc ttg tcc acg  
1603  
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490 495 500

cat gac acc aaa cgt ggc gaa gat acc cgc gcc cgc atc atc tcc ctg  
1651  
His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala Arg Ile Ile Ser Leu  
505 510 515

tct gaa gtc ccc gat atg tac tcc gag ctg gtc aat cgt gtt ttc gcg  
1699  
Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val Asn Arg Val Phe Ala  
520 525 530

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535 540 545

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 Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile Thr Asp Ala Leu Arg  
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 Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile Arg Glu Ala Ser Thr  
 570 575 580  
  
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 1891  
 Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe Glu Ala Ala Val Cys  
 585 590 595  
  
 gat tgg gtg gaa gcg ctt ttc gac gga ccc tcc acc tca cta atc acc  
 1939  
 Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser Thr Ser Leu Ile Thr  
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 1987  
 Glu Phe Val Ser His Ile Asn Arg Gly Ser Val Gln Ile Ser Leu Gly  
 615 620 625  
  
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 Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile Pro Asp Thr Tyr Gln  
 630 635 640 645  
  
 gga act gag ttt tta gaa gac tcc ctg gta gat ccc gat aac cga cgc  
 2083  
 Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp Pro Asp Asn Arg Arg  
 650 655 660  
  
 ttt gtt gat tac acc gcc aga gaa caa gtc ctg gag cgc ctg caa acc  
 2131  
 Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu Glu Arg Leu Gln Thr  
 665 670 675  
  
 tgg gat tgg acg cag gtt aat tcg gta gaa gac ttg gtg gat aac gcc  
 2179  
 Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp Leu Val Asp Asn Ala  
 680 685 690  
  
 gac atc gcc aaa atg gcc gtg gtc cat aaa tcc ctc gag ttg cgt gct  
 2227  
 Asp Ile Ala Lys Met Ala Val Val His Lys Ser Leu Glu Leu Arg Ala  
 695 700 705  
  
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 2275  
 Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His Gln Ala Val Phe Gly  
 710 715 720 725  
  
 gaa ggt cgc gca gaa tcc cac atc atg ggc atc gcc cgc ggt aca gac  
 2323  
 Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile Ala Arg Gly Thr Asp  
 730 735 740



cga aac cac ctc aac atc att gct ctt gct acc cgt cga cca ctg atc  
2371

Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr Arg Arg Pro Leu Ile  
745 750 755

ttg gaa gac cgt ggc gga tgg tat gac acc acc gtc acg ctt cct ggt  
2419

Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr Val Thr Leu Pro Gly  
760 765 770

gga caa tgg gaa gac agg ctc acc ggg caa cgc ttc agt ggt gtt gtc  
2467

Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg Phe Ser Gly Val Val  
775 780 785

cca gcc acc gat ttg ttc tca cat cta ccc gta tct ttg ttg gtt tta  
2515

Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val Ser Leu Leu Val Leu  
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2556

Val Pro Asp Ser Glu Phe  
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<211> 811

<212> PRT

<213> Corynebacterium glutamicum

<400> 1144

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Gln Leu Pro Tyr Leu Lys Lys Leu Gly Ile Ser His Leu Tyr Leu Ser  
35 40 45

Pro Ile Phe Thr Ala Met Pro Asp Ser Asn His Gly Tyr Asp Val Ile  
50 55 60

Asp Pro Thr Thr Ile Asn Glu Glu Leu Gly Gly Met Glu Gly Leu Arg  
65 70 75 80

Asp Leu Ala Ala Ala Thr His Glu Leu Gly Met Gly Ile Ile Ile Asp  
85 90 95

Ile Val Pro Asn His Leu Gly Val Ala Val Pro His Leu Asn Pro Trp  
100 105 110

Trp Trp Asp Val Leu Lys Asn Gly Lys Asp Ser Ala Phe Glu Phe Tyr  
115 120 125

Phe Asp Ile Asp Trp His Glu Asp Asn Gly Ser Gly Gly Lys Leu Gly  
130 135 140

Met Pro Ile Leu Gly Ala Glu Gly Asp Glu Asp Lys Leu Glu Phe Ala  
145 150 155 160

Glu Leu Asp Gly Glu Lys Val Leu Lys Tyr Phe Asp His Leu Phe Pro  
 165 170 175  
 Ile Ala Pro Gly Thr Glu Glu Gly Thr Pro Gln Glu Val Tyr Lys Arg  
 180 185 190  
 Gln His Tyr Arg Leu Gln Phe Trp Arg Asp Gly Val Ile Asn Phe Arg  
 195 200 205  
 Arg Phe Phe Ser Val Asn Thr Leu Ala Gly Ile Arg Gln Glu Asp Pro  
 210 215 220  
 Leu Val Phe Glu His Thr His Arg Leu Leu Arg Glu Leu Val Ala Glu  
 225 230 235 240  
 Asp Leu Ile Asp Gly Val Arg Val Asp His Pro Asp Gly Leu Ser Asp  
 245 250 255  
 Pro Phe Gly Tyr Leu His Arg Leu Arg Asp Leu Ile Gly Pro Asp Arg  
 260 265 270  
 Trp Leu Ile Ile Glu Lys Ile Leu Ser Val Asp Glu Pro Leu Asp Pro  
 275 280 285  
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 290 295 300  
 Asp Gly Val Phe Ile Ser Arg Glu Ser Glu Asp Lys Phe Ser Met Leu  
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 Ala Leu Thr His Ser Gly Ser Thr Trp Asp Glu Arg Ala Leu Lys Ser  
 325 330 335  
 Thr Glu Glu Ser Leu Lys Arg Val Val Ala Gln Gln Glu Leu Ala Ala  
 340 345 350  
 Glu Ile Leu Arg Leu Ala Arg Ala Met Arg Arg Asp Asn Phe Ser Thr  
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 Ala Gly Thr Asn Val Thr Glu Asp Lys Leu Ser Glu Thr Ile Ile Glu  
 370 375 380  
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 385 390 395 400  
 Arg Thr Thr Ala Thr Val Ile Ala Glu Met Ser Lys Arg Phe Pro Ser  
 405 410 415  
 Arg Arg Asp Ala Leu Asp Leu Ile Ala Ala Ala Leu Leu Gly Asn Gly  
 420 425 430  
 Glu Ala Lys Ile Arg Phe Ala Gln Val Cys Gly Ala Val Met Ala Lys  
 435 440 445  
 Gly Val Glu Asp Thr Thr Phe Tyr Arg Ala Ser Arg Leu Val Ala Leu  
 450 455 460  
 Gln Glu Val Gly Gly Ala Pro Gly Arg Phe Gly Val Ser Ala Ala Glu  
 465 470 475 480

Phe His Leu Leu Gln Glu Glu Arg Ser Leu Leu Trp Pro Arg Thr Met  
 485 490 495  
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Gly Glu Asp Thr Arg Ala  
 500 505 510  
 Arg Ile Ile Ser Leu Ser Glu Val Pro Asp Met Tyr Ser Glu Leu Val  
 515 520 525  
 Asn Arg Val Phe Ala Val Leu Pro Ala Pro Asp Gly Ala Thr Gly Ser  
 530 535 540  
 Phe Leu Leu Gln Asn Leu Leu Gly Val Trp Pro Ala Asp Gly Val Ile  
 545 550 555 560  
 Thr Asp Ala Leu Arg Asp Arg Phe Arg Glu Tyr Ala Leu Lys Ala Ile  
 565 570 575  
 Arg Glu Ala Ser Thr Lys Thr Thr Trp Val Asp Pro Asn Glu Ser Phe  
 580 585 590  
 Glu Ala Ala Val Cys Asp Trp Val Glu Ala Leu Phe Asp Gly Pro Ser  
 595 600 605  
 Thr Ser Leu Ile Thr Glu Phe Val Ser His Ile Asn Arg Gly Ser Val  
 610 615 620  
 Gln Ile Ser Leu Gly Arg Lys Leu Leu Gln Met Val Gly Ala Gly Ile  
 625 630 635 640  
 Pro Asp Thr Tyr Gln Gly Thr Glu Phe Leu Glu Asp Ser Leu Val Asp  
 645 650 655  
 Pro Asp Asn Arg Arg Phe Val Asp Tyr Thr Ala Arg Glu Gln Val Leu  
 660 665 670  
 Glu Arg Leu Gln Thr Trp Asp Trp Thr Gln Val Asn Ser Val Glu Asp  
 675 680 685  
 Leu Val Asp Asn Ala Asp Ile Ala Lys Met Ala Val Val His Lys Ser  
 690 695 700  
 Leu Glu Leu Arg Ala Glu Phe Arg Ala Ser Phe Val Gly Gly Asp His  
 705 710 715 720  
 Gln Ala Val Phe Gly Glu Gly Arg Ala Glu Ser His Ile Met Gly Ile  
 725 730 735  
 Ala Arg Gly Thr Asp Arg Asn His Leu Asn Ile Ile Ala Leu Ala Thr  
 740 745 750  
 Arg Arg Pro Leu Ile Leu Glu Asp Arg Gly Gly Trp Tyr Asp Thr Thr  
 755 760 765  
 Val Thr Leu Pro Gly Gly Gln Trp Glu Asp Arg Leu Thr Gly Gln Arg  
 770 775 780  
 Phe Ser Gly Val Val Pro Ala Thr Asp Leu Phe Ser His Leu Pro Val  
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 Ser Leu Leu Val Leu Val Pro Asp Ser Glu Phe

805

810

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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1930)  
<223> RXA02645
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											atg ctc aaa gac ttg	115				
											Met Leu Lys Asp Leu					
											1	5				
acc ggc ctg agg gag ttg gta ttg cgt gag atg tgc cat agc atc tca																163
Thr Gly Leu Arg Glu Leu Val Leu Arg Glu Met Cys His Ser Ile Ser																
10 15 20																
cat ctt agc tcg cca acc ggc agc att ttc act agc ctg gtg gcc atg																211
His Leu Ser Ser Pro Thr Gly Ser Ile Phe Thr Ser Leu Val Ala Met																
25 30 35																
ttg acc tcg caa agc ttt tca gtg tgg gct cca ctt ccc cac gat gta																259
Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro Leu Pro His Asp Val																
40 45 50																
cat ctg atc ctc aac ggc gaa acc ctc ccc atg cac aaa acg gag ggc																307
His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met His Lys Thr Glu Gly																
55 60 65																
agc tgg tgg cgc gcc gag atc gcg ccc aag gcc ggc gat cgt tac ggt																355
Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala Gly Asp Arg Tyr Gly																
70 75 80 85																
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Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys Thr Leu Pro Asp Pro																
90 95 100																
cgc tcc aca tct caa cca gac ggg gtt cat ggt tta agt gaa gtc tcc																451
Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly Leu Ser Glu Val Ser																
105 110 115																
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Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp Thr Gly Arg Ile Leu																
120 125 130																
cct ggc tcg gtg tta tat gag ctg cat gtg ggc acc ttt agt gaa gat																547
Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly Thr Phe Ser Glu Asp																
135 140 145																
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Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro Tyr Leu Arg Asp Leu																
150 155 160 165																
ggc gtg acc gcc atc gaa ctt tta ccc gtg cag ccc ttt ggc ggc aac																643

Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln Pro Phe Gly Gly Asn	
170	175 180
cgc aat tgg ggc tac gac ggg gtg ctg tgg cac gcc gtc cat gca ggc	691
Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His Ala Val His Ala Gly	
185	190 195
tac ggc ggt ccg gcg ggc ttg aaa aag ctt atc gac gcc tcc cac cag	739
Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile Asp Ala Ser His Gln	
200	205 210
gcc ggc atc gcc gtc tac tta gac gtc gtg tac aac cac ttc ggc ccc	787
Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr Asn His Phe Gly Pro	
215	220 225
gac ggc aac tac aac ggg caa ttt ggc ccc tac acc tct ggc ggc agc	835
Asp Gly Asn Tyr Asn Gln Phe Gly Pro Tyr Thr Ser Gly Gly Ser	
230	235 240 245
acc ggc tgg ggc gac gtg gtc aac atc aac ggc cat gat tca gat gaa	883
Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly His Asp Ser Asp Glu	
250	255 260
gtc cgc aat tat att ctc gac gcc gca cgc cag tgg ttc gaa gat ttt	931
Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln Trp Phe Glu Asp Phe	
265	270 275
cac gtt gat ggg ctc cgc ctc gat gcg gtg cat tct ctc gat gat cgc	979
His Val Asp Gly Leu Arg Leu Asp Ala Val His Ser Leu Asp Asp Arg	
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ggc gcc tat tcc cta ctt gcg cag ctg acc atg gtg gcc gag gat gtc	
1027	
Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met Val Ala Glu Asp Val	
295	300 305
tcc gca caa aca ggc atc cca cgc tca ttg att gca gaa tct gaa ctc	
1075	
Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile Ala Glu Ser Glu Leu	
310	315 320 325
aat gac ccc aag ttc gtt acc tcc cgc gag gcc ggc ggt ttt ggc ctg	
1123	
Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala Gly Gly Phe Gly Leu	
330	335 340
gat gca cag tgg gtt gac gat atc cac cac gcc ctc cat gcc ctc gtt	
1171	
Asp Ala Gln Trp Val Asp Asp Ile His His Ala Leu His Ala Leu Val	
345	350 355
tct ggc gaa cgc aat ggt tat tac agc gat ttc gga tct gtc gac aca	
1219	
Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe Gly Ser Val Asp Thr	
360	365 370
tta gcc aaa acc ctg cgt gaa gta ttt gaa cac acc gga aac tac tcc	
1267	
Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His Thr Gly Asn Tyr Ser	
375	380 385

gag ctg att tac agc ttc act tcc ccc acc gtc acc gac acc tcc aca  
1891  
Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val Thr Asp Thr Ser Thr  
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1953

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Ser Leu Val Ala Met Leu Thr Ser Gln Ser Phe Ser Val Trp Ala Pro  
35 40 45

Leu Pro His Asp Val His Leu Ile Leu Asn Gly Glu Thr Leu Pro Met  
50 55 60

His Lys Thr Glu Gly Ser Trp Trp Arg Ala Glu Ile Ala Pro Lys Ala  
65 70 75 80

Gly Asp Arg Tyr Gly Phe Ser Leu Phe Asp Gly Ser Ser Trp Ser Lys  
85 90 95

Thr Leu Pro Asp Pro Arg Ser Thr Ser Gln Pro Asp Gly Val His Gly  
100 105 110

Leu Ser Glu Val Ser Asp Asp Ser Tyr Leu Trp Gly Asp Gln Gln Trp  
115 120 125

Thr Gly Arg Ile Leu Pro Gly Ser Val Leu Tyr Glu Leu His Val Gly  
130 135 140

Thr Phe Ser Glu Asp Gly Thr Phe Glu Gly Val Val Asp Lys Leu Pro  
145 150 155 160

Tyr Leu Arg Asp Leu Gly Val Thr Ala Ile Glu Leu Leu Pro Val Gln  
165 170 175

Pro Phe Gly Gly Asn Arg Asn Trp Gly Tyr Asp Gly Val Leu Trp His  
180 185 190

Ala Val His Ala Gly Tyr Gly Gly Pro Ala Gly Leu Lys Lys Leu Ile  
195 200 205

Asp Ala Ser His Gln Ala Gly Ile Ala Val Tyr Leu Asp Val Val Tyr  
210 215 220

acg tac cgc gga cgc aac cac ggc cgc cct gtg cac ccc gat atc acc  
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cct gcc tcg cgc ttt gtc acc tac acc acc acc cat gat cag acc ggc  
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 Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr His Asp Gln Thr Gly  
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aac cgc gca atc ggc gac cgt cct tcc acg act ctc acc ccg gaa cag  
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 Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr Leu Thr Pro Glu Gln  
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 1459  
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 440 445 450

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 Lys Arg Glu Phe Ala Arg Leu Gly Trp Asn Ala Asp Asp Ile Pro Ser  
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ccc gag ctg gaa tcc acc ttc acc tcc tcc aaa ctc gat tgg gag ttc  
 1651  
 Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys Leu Asp Trp Glu Phe  
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 520 525 530

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 535 540 545

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 1843  
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 570 575 580

Asn His Phe Gly Pro Asp Gly Asn Tyr Asn Gly Gln Phe Gly Pro Tyr  
 225 230 235 240  
 Thr Ser Gly Gly Ser Thr Gly Trp Gly Asp Val Val Asn Ile Asn Gly  
 245 250 255  
 His Asp Ser Asp Glu Val Arg Asn Tyr Ile Leu Asp Ala Ala Arg Gln  
 260 265 270  
 Trp Phe Glu Asp Phe His Val Asp Gly Leu Arg Leu Asp Ala Val His  
 275 280 285  
 Ser Leu Asp Asp Arg Gly Ala Tyr Ser Leu Leu Ala Gln Leu Thr Met  
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 Val Ala Glu Asp Val Ser Ala Gln Thr Gly Ile Pro Arg Ser Leu Ile  
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 Ala Glu Ser Glu Leu Asn Asp Pro Lys Phe Val Thr Ser Arg Glu Ala  
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 340 345 350  
 Leu His Ala Leu Val Ser Gly Glu Arg Asn Gly Tyr Tyr Ser Asp Phe  
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 Gly Ser Val Asp Thr Leu Ala Lys Thr Leu Arg Glu Val Phe Glu His  
 370 375 380  
 Thr Gly Asn Tyr Ser Thr Tyr Arg Gly Arg Asn His Gly Arg Pro Val  
 385 390 395 400  
 His Pro Asp Ile Thr Pro Ala Ser Arg Phe Val Thr Tyr Thr Thr Thr  
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 His Asp Gln Thr Gly Asn Arg Ala Ile Gly Asp Arg Pro Ser Thr Thr  
 420 425 430  
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 Pro Tyr Thr Pro Met Leu Phe Met Gly Glu Glu Phe Gly Ala Thr Thr  
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 Pro Phe Ala Phe Phe Cys Ser His Thr Asp Pro Glu Leu Asn Arg Leu  
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 485 490 495  
 Asp Asp Ile Pro Ser Pro Glu Leu Glu Ser Thr Phe Thr Ser Ser Lys  
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 515 520 525  
 Lys Gln Leu Leu His Leu Arg His Thr Leu Gly Phe Ser Gln Pro Asn  
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Leu Leu Thr Leu Glu Val Glu His Gly Glu Asn Trp Leu Ser Met Ala  
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Asn Gly Arg Gly Arg Ile Leu Ala Asn Phe Ser Asp Asp Thr Ile Thr  
565 570 575

Val Pro Leu Gly Gly Glu Leu Ile Tyr Ser Phe Thr Ser Pro Thr Val  
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Arg Asn  
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<211> 832

<212> DNA

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<223> RXN02355

<400> 1147

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Met Ser Ser Ile Ser  
1 5

cgc aag acc ggc gcg tca ctt gca gcc acc aca ctg ttg gca gcg atc 163  
Arg Lys Thr Gly Ala Ser Leu Ala Ala Thr Thr Leu Leu Ala Ala Ile  
10 15 20

gca ctg gcc ggt tgt agt tca gac tca agc tcc gac tcc aca gat tcc 211  
Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser Asp Ser Thr Asp Ser  
25 30 35

acc gct agc gaa ggc gca gac agc cgc ggc ccc atc acc ttt gcg atg 259  
Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro Ile Thr Phe Ala Met  
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ggc aaa aac gac acc gac aaa gtc att ccg atc atc gac cgc tgg aac 307  
Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile Ile Asp Arg Trp Asn  
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70 75 80 85

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Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser Leu Gln Ala Gly Asn  
90 95 100

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Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile Trp Thr Ala Asp Phe  
105 110 115

gcg gca aac caa tgg ctc gca cca ctt gaa ggc gac ctc gag gta gac 499  
 Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly Asp Leu Glu Val Asp  
                   120                  125                  130

acc tcc gga ctg ctg caa tcc acc gtg gat tcc gca acc tac aac ggc 547  
 Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser Ala Thr Tyr Asn Gly  
                   135                  140                  145

acc ctc tac gca ctg cca cag aac acc aac ggc cag cta ctg ttc cgc 595  
 Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly Gln Leu Leu Phe Arg  
                   150                  155                  160                  165

aac acc gaa atc atc cca gaa gca cca gca aac tgg gct gac ctc gtg 643  
 Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn Trp Ala Asp Leu Val  
                                   170                                  175                                  180

gaa tcc tgc acg ctt gct gaa gaa gca ggc gtt gat tgc ctg acc act 691  
 Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val Asp Cys Leu Thr Thr  
                   185                                  190                                  195

cag ctc aag cag tac gaa ggc ctt tca gtg aac acc atc ggc ttc atc 739  
 Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn Thr Ile Gly Phe Ile  
                   200                                  205                                  210

gaa ggt tgg gga ggc agc gtc cta gac gat gac ggc aaa cgt cac cgt 787  
 Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp Gly Lys Arg His Arg  
                   215                                  220                                  225

aga cag cac gac ggc aag gca ggc ctt caa gcg ctt gtc gac ggc 832  
 Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala Leu Val Asp Gly  
                   230                                  235                                  240

&lt;210&gt; 1148

&lt;211&gt; 244

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1148

Met Ser Ser Ile Ser Arg Lys Thr Gly Ala Ser Leu Ala Ala Thr Thr  
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Leu Leu Ala Ala Ile Ala Leu Ala Gly Cys Ser Ser Asp Ser Ser Ser  
                   20                                  25                                  30

Asp Ser Thr Asp Ser Thr Ala Ser Glu Gly Ala Asp Ser Arg Gly Pro  
                   35                                  40                                  45

Ile Thr Phe Ala Met Gly Lys Asn Asp Thr Asp Lys Val Ile Pro Ile  
                   50                                  55                                  60

Ile Asp Arg Trp Asn Glu Ala His Pro Asp Glu Gln Val Thr Leu Asn  
                   65                                  70                                  75                                  80

Glu Leu Ala Gly Glu Ala Asp Ala Gln Arg Glu Thr Leu Val Gln Ser  
                                   85                                  90                                  95

Leu Gln Ala Gly Asn Ser Asp Tyr Asp Val Met Ala Leu Asp Val Ile  
                   100                                  105                                  110

Trp Thr Ala Asp Phe Ala Ala Asn Gln Trp Leu Ala Pro Leu Glu Gly

115	120	125
Asp Leu Glu Val Asp Thr Ser Gly Leu Leu Gln Ser Thr Val Asp Ser		
130	135	140
Ala Thr Tyr Asn Gly Thr Leu Tyr Ala Leu Pro Gln Asn Thr Asn Gly		
145	150	155
Gln Leu Leu Phe Arg Asn Thr Glu Ile Ile Pro Glu Ala Pro Ala Asn		
165	170	175
Trp Ala Asp Leu Val Glu Ser Cys Thr Leu Ala Glu Glu Ala Gly Val		
180	185	190
Asp Cys Leu Thr Thr Gln Leu Lys Gln Tyr Glu Gly Leu Ser Val Asn		
195	200	205
Thr Ile Gly Phe Ile Glu Gly Trp Gly Gly Ser Val Leu Asp Asp Asp		
210	215	220
Gly Lys Arg His Arg Arg Gln His Asp Gly Lys Ala Gly Leu Gln Ala		
225	230	235
240		
Leu Val Asp Gly		

&lt;210&gt; 1149

&lt;211&gt; 609

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(586)

&lt;223&gt; RXN02909

&lt;400&gt; 1149

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caacgcgaat gaaaacgaac agcgagcagg tctataccca cgacgtcaac gtgtgggcta 60
atagtttcct ggattgtttg gcacagtcgg gagaaaactc atg aac cgc gca cga 115
                                         Met Asn Arg Ala Arg
                                         1 5
atc gcg acc ata ggc gtt ctt ccg ctt gct tta ctg ctg gcg tcc tgt 163
Ile Ala Thr Ile Gly Val Leu Pro Leu Ala Leu Leu Leu Ala Ser Cys
                        10 15 20
ggg tca gac acc gtg gaa atg aca gat tcc acc tgg ttg gtg acc aat 211
Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr Trp Leu Val Thr Asn
                        25 30 35
att tac acc gat cca gat gag tcg aat tcg atc agt aat ctt gtc att 259
Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile Ser Asn Leu Val Ile
                        40 45 50
tcc cag ccc agc tta gat ttt ggc aat tct tcc ctg tct ggt ttc act 307
Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser Ser Gly Phe Thr
                        55 60 65
ggc tgt gtg cct ttt acg ggg cgt gcg gaa ttc ttc caa aat ggt gag 355

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Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe Phe Gln Asn Gly Glu  
 70 75 80 85  
 caa agc tct gtt ctg gat gcc gat tat gtg acc ttg tct tcc ctg gat 403  
 Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr Leu Ser Ser Leu Asp  
 90 95 100  
 ttc gat aaa ctt ccc gat gat tgc caa gga caa gaa ctc aaa gtt cat 451  
 Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln Glu Leu Lys Val His  
 105 110 115  
 aac gag ctg gtt gat ctt ctg cct ggt tct ttt gaa atc tcc agg act 499  
 Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe Glu Ile Ser Arg Thr  
 120 125 130  
 tct ggt tca gaa atc ttg ctg act agc gat gtc gat gaa ctc gat cgg 547  
 Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val Asp Glu Leu Asp Arg  
 135 140 145  
 cca gca atc cgc ttg gtg tcc tgg atc gcg ccg aca tct taaggtgccca 596  
 Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro Thr Ser  
 150 155 160  
 gggctttaaaa gtg 609  
  
 <210> 1150  
 <211> 162  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
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 Leu Leu Ala Ser Cys Gly Ser Asp Thr Val Glu Met Thr Asp Ser Thr  
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 Trp Leu Val Thr Asn Ile Tyr Thr Asp Pro Asp Glu Ser Asn Ser Ile  
 35 40 45  
 Ser Asn Leu Val Ile Ser Gln Pro Ser Leu Asp Phe Gly Asn Ser Ser  
 50 55 60  
 Leu Ser Gly Phe Thr Gly Cys Val Pro Phe Thr Gly Arg Ala Glu Phe  
 65 70 75 80  
 Phe Gln Asn Gly Glu Gln Ser Ser Val Leu Asp Ala Asp Tyr Val Thr  
 85 90 95  
 Leu Ser Ser Leu Asp Phe Asp Lys Leu Pro Asp Asp Cys Gln Gly Gln  
 100 105 110  
 Glu Leu Lys Val His Asn Glu Leu Val Asp Leu Leu Pro Gly Ser Phe  
 115 120 125  
 Glu Ile Ser Arg Thr Ser Gly Ser Glu Ile Leu Leu Thr Ser Asp Val  
 130 135 140  
 Asp Glu Leu Asp Arg Pro Ala Ile Arg Leu Val Ser Trp Ile Ala Pro  
 145 150 155 160

Thr Ser

&lt;210&gt; 1151

&lt;211&gt; 1590

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1567)

&lt;223&gt; RXS00349

&lt;400&gt; 1151

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gtgattggac	tcttttttct	tgcaaaatgt	tttccagcgg	atg	ttg	agt	ttt	gcg	115
				Met	Leu	Ser	Phe	Ala	
				1				5	

acc	ctt	cgt	ggc	cgc	att	tca	aca	ggt	gac	gct	gca	aaa	gcc	gca	cct	163
Thr	Leu	Arg	Gly	Arg	Ile	Ser	Thr	Val	Asp	Ala	Ala	Lys	Ala	Ala	Pro	
			10						15					20		

ccg	cca	tcg	cca	cta	gcc	ccg	att	gat	ctc	act	gac	cat	agt	caa	gtg	211
Pro	Pro	Ser	Pro	Leu	Ala	Pro	Ile	Asp	Leu	Thr	Asp	His	Ser	Gln	Val	
			25					30					35			

gcc	ggt	gtg	atg	aat	ttg	gct	gcg	aga	att	ggc	gat	att	ttg	ctt	tct	259
Ala	Gly	Val	Met	Asn	Leu	Ala	Ala	Arg	Ile	Gly	Asp	Ile	Leu	Leu	Ser	
		40				45					50					

tca	ggt	acg	tca	aat	agt	gac	acc	aag	gta	caa	ggt	cga	gca	gtg	acc	307
Ser	Gly	Thr	Ser	Asn	Ser	Asp	Thr	Lys	Val	Gln	Val	Arg	Ala	Val	Thr	
	55					60				65						

tct	gcg	tac	ggt	ttg	tac	tac	acg	cac	gtg	gat	atc	acg	ttg	aat	acg	355
Ser	Ala	Tyr	Gly	Leu	Tyr	Tyr	Thr	His	Val	Asp	Ile	Thr	Leu	Asn	Thr	
70					75					80					85	

atc	acc	atc	ttc	acc	aac	atc	ggt	gtg	gag	agg	aag	atg	ccg	gtc	aac	403
Ile	Thr	Ile	Phe	Thr	Asn	Ile	Gly	Val	Glu	Arg	Lys	Met	Pro	Val	Asn	
				90					95					100		

gtg	ttt	cat	ggt	gta	ggc	aag	ttg	gac	acc	aac	ttc	tcc	aaa	ctg	tct	451
Val	Phe	His	Val	Val	Gly	Lys	Leu	Asp	Thr	Asn	Phe	Ser	Lys	Leu	Ser	
			105					110					115			

gag	ggt	gac	cgt	ttg	atc	cgt	tcc	att	cag	gct	ggt	gcg	acc	ccg	cct	499
Glu	Val	Asp	Arg	Leu	Ile	Arg	Ser	Ile	Gln	Ala	Gly	Ala	Thr	Pro	Pro	
		120					125					130				

gag	ggt	gcc	gag	aaa	atc	ctg	gac	gag	ttg	gag	caa	tcc	cct	gcg	tct	547
Glu	Val	Ala	Glu	Lys	Ile	Leu	Asp	Glu	Leu	Glu	Gln	Ser	Pro	Ala	Ser	
		135				140					145					

tat	ggt	ttc	cct	ggt	gcg	ttg	ctt	ggc	tgg	gca	atg	atg	ggt	ggt	gct	595
Tyr	Gly	Phe	Pro	Val	Ala	Leu	Leu	Gly	Trp	Ala	Met	Met	Gly	Gly	Ala	
150					155					160					165	

gtt gct gtg ctg ttg ggt ggt gga tgg cag gtt tcc cta att gct ttt	643
Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val Ser Leu Ile Ala Phe	
170 175 180	
att acc gcg ttc acg atc att gcc acg acg tca ttt ttg gga aag aag	691
Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys	
185 190 195	
ggt ttg cct act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg	739
Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr	
200 205 210	
ctg cct gca tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag	787
Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu	
215 220 225	
atc aaa ccg agc cag atc atc gca tct gga att gtt gtg ctg ttg gca	835
Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala	
230 235 240 245	
ggt ttg aca ctc gtg caa tct ctg cag gac ggc atc acg ggc gct ccg	883
Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro	
250 255 260	
gtg aca gca agt gca cga ttt ttc gaa aca ctc ctg ttt acc ggc ggc	931
Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly	
265 270 275	
att gtt gct ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat	979
Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His	
280 285 290	
gtc atg ttg cct gcc atg gag tcc gct gca gca cct aat tat tcg tct	
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Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser	
295 300 305	
aca ttc gcc cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca	
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Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala	
310 315 320 325	
gtg ggt tgt tac gcg gag tgg tcc tcg gtg att att gcg ggg ctt act	
1123	
Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr	
330 335 340	
gcg ctg atg ggt tct gcg ttt tat tac ctc ttc gtt gtt tat tta ggc	
1171	
Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly	
345 350 355	
ccc gtc tct gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt	
1219	
Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly	
360 365 370	
ggt ttg ctt gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att	
1267	
Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile	

375                      380                      385  
 gcc ggc atc aca cca atg ctt cca ggt cta gca att tac cgc gga atg  
 1315  
 Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met  
 390                      395                      400                      405  
 tac gcc acc ctg aat gat caa aca ctc atg ggt ttc acc aac att gcg  
 1363  
 Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala  
                     410                      415                      420  
 gtt gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt  
 1411  
 Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly  
                     425                      430                      435  
 gag tgg att gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac  
 1459  
 Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr  
                     440                      445                      450  
 cgt gca ttt acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag  
 1507  
 Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu  
                     455                      460                      465  
 cag aat cag cgc cgg cag aga aaa cgt cca aag act aat cag aga ttc  
 1555  
 Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe  
 470                      475                      480                      485  
 ggt aat aaa agg taaaaatcaa cctgcttagg cgt  
 1590  
 Gly Asn Lys Arg

<210> 1152  
 <211> 489  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 1152  
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 Ala Lys Ala Ala Pro Pro Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr  
                     20                    25                    30  
 Asp His Ser Gln Val Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly  
                     35                    40                    45  
 Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln  
                     50                    55                    60  
 Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp  
   65                    70                    75                    80  
 Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg  
                     85                    90                    95

Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn  
 100 105 110  
 Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala  
 115 120 125  
 Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu  
 130 135 140  
 Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala  
 145 150 155 160  
 Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val  
 165 170 175  
 Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser  
 180 185 190  
 Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly  
 195 200 205  
 Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu  
 210 215 220  
 Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile  
 225 230 235 240  
 Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly  
 245 250 255  
 Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu  
 260 265 270  
 Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu  
 275 280 285  
 Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala  
 290 295 300  
 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr  
 305 310 315 320  
 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile  
 325 330 335  
 Ile Ala Gly Leu Thr Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe  
 340 345 350  
 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala  
 355 360 365  
 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro  
 370 375 380  
 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala  
 385 390 395 400  
 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly  
 405 410 415



Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala  
                     420                    425                    430  
 Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro  
                     435                    440                    445  
 Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe  
                     450                    455                    460  
 Gln Glu Glu Ala Glu Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys  
                     465                    470                    475                    480  
 Thr Asn Gln Arg Phe Gly Asn Lys Arg  
                     485

&lt;210&gt; 1153

&lt;211&gt; 440

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(417)

&lt;223&gt; RXS03183

&lt;400&gt; 1153

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 Glu Ala Glu Ala Thr Ala Gly Lys Phe Glu Val Gln Pro Leu Val Gly  
     1                    5                    10                    15  
 aaa gac ggc gtc ggc gta tcc acc ctt ggt ggc tac aac aac ggc atc 96  
 Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile  
                     20                    25                    30  
 aac gtc aac tcc gaa aac aag gca acc gcc cgc gac ttc atc gaa ttc 144  
 Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe  
                     35                    40                    45  
 atc atc aac gaa gag aac caa acc tgg ttc gcg gac aac tcc ttc cca 192  
 Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro  
     50                    55                    60  
 cca gtt ctg gca tcc atc tac gat gat gag tcc ctt gtt gag cag tac 240  
 Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr  
     65                    70                    75                    80  
 cca tac ctg cca gca ctg aag gaa tcc ctg gaa aac gca gca cca cgc 288  
 Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg  
                     85                    90                    95  
 cca gtg tct cct ttc tac cca gcc atc tcc aag gca atc cag gac aac 336  
 Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn  
                     100                    105                    110  
 gcc tac gca gcg ctt aac ggc aac gtc gac gtt gac cag gca acc acc 384  
 Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr  
                     115                    120                    125  
 gat atg aag gca gcg atc gaa aac gct tcc agc tagttcggta atttagttca 437  
 Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser

130

135

ttc

440

&lt;210&gt; 1154

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 1154

Glu Ala Glu Ala Thr Ala Gly Lys Phe Glu Val Gln Pro Leu Val Gly  
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Lys Asp Gly Val Gly Val Ser Thr Leu Gly Gly Tyr Asn Asn Gly Ile  
 20 25 30

Asn Val Asn Ser Glu Asn Lys Ala Thr Ala Arg Asp Phe Ile Glu Phe  
 35 40 45

Ile Ile Asn Glu Glu Asn Gln Thr Trp Phe Ala Asp Asn Ser Phe Pro  
 50 55 60

Pro Val Leu Ala Ser Ile Tyr Asp Asp Glu Ser Leu Val Glu Gln Tyr  
 65 70 75 80

Pro Tyr Leu Pro Ala Leu Lys Glu Ser Leu Glu Asn Ala Ala Pro Arg  
 85 90 95

Pro Val Ser Pro Phe Tyr Pro Ala Ile Ser Lys Ala Ile Gln Asp Asn  
 100 105 110

Ala Tyr Ala Ala Leu Asn Gly Asn Val Asp Val Asp Gln Ala Thr Thr  
 115 120 125

Asp Met Lys Ala Ala Ile Glu Asn Ala Ser Ser  
 130 135

&lt;210&gt; 1155

&lt;211&gt; 1212

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1189)

&lt;223&gt; RXC00874

&lt;400&gt; 1155

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tctggtttga tctcaccgcc gatgaaaagg acgatatgga atg agc att ggc caa 115  
 Met Ser Ile Gly Gln  
 1 5

cac atc atc acc gag cgt ttc tac ggc gcc aag tcc cac acc atc gac 163  
 His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys Ser His Thr Ile Asp  
 10 15 20

aac gta gat att gtg ttg tcc cgc gaa tgt ggc gag aac act ttg gct 211

Asn	Val	Asp	Ile	Val	Leu	Ser	Arg	Glu	Cys	Gly	Glu	Asn	Thr	Leu	Ala		
			25					30					35				
gta	gtg	cgc	atc	aac	aat	gcg	ctg	tat	cag	ttg	ttg	gtc	aat	gat	gat	259	
Val	Val	Arg	Ile	Asn	Asn	Ala	Leu	Tyr	Gln	Leu	Leu	Val	Asn	Asp	Asp		
		40					45					50					
ggc	aaa	gat	gtt	ctc	aac	gac	cac	gta	gaa	gag	gtc	ggg	gcg	agt	ttc	307	
Gly	Lys	Asp	Val	Leu	Asn	Asp	His	Val	Glu	Glu	Val	Gly	Ala	Ser	Phe		
	55					60					65						
gga	gca	tgg	act	ggc	agc	tct	gct	ttt	ccc	att	ggc	cct	ttc	act	cca	355	
Gly	Ala	Trp	Thr	Gly	Ser	Ser	Ala	Phe	Pro	Ile	Gly	Pro	Phe	Thr	Pro		
	70				75				80						85		
ctc	ggc	aca	gaa	caa	tcc	aat	agc	tct	ttc	atc	acc	gcc	gac	aat	aaa	403	
Leu	Gly	Thr	Glu	Gln	Ser	Asn	Ser	Ser	Phe	Ile	Thr	Ala	Asp	Asn	Lys		
				90					95					100			
gcg	atc	gtg	aaa	tac	ttc	cgc	aaa	tta	gaa	tcc	ggg	caa	aac	ccc	gat	451	
Ala	Ile	Val	Lys	Tyr	Phe	Arg	Lys	Leu	Glu	Ser	Gly	Gln	Asn	Pro	Asp		
			105					110					115				
gtg	gag	cta	att	tct	aaa	att	tcc	tcc	tgc	ccc	aac	atc	gcg	ccc	atc	499	
Val	Glu	Leu	Ile	Ser	Lys	Ile	Ser	Ser	Cys	Pro	Asn	Ile	Ala	Pro	Ile		
		120					125					130					
ctg	ggg	ttt	tcc	tcc	gct	gag	atc	tcc	ggg	gct	aac	tac	acc	ctg	gtc	547	
Leu	Gly	Phe	Ser	Ser	Ala	Glu	Ile	Ser	Gly	Ala	Asn	Tyr	Thr	Leu	Val		
	135					140					145						
atg	gag	cag	cag	tac	gtt	cca	ggg	ttg	gat	ggc	tgg	tca	cac	gag	ctg	595	
Met	Ala	Gln	Gln	Tyr	Val	Pro	Gly	Leu	Asp	Gly	Trp	Ser	His	Ala	Leu		
	150				155					160					165		
act	act	acc	tct	ggc	agc	ttt	gca	gag	gat	gca	gaa	aag	atc	ggc	gaa	643	
Thr	Thr	Thr	Ser	Gly	Ser	Phe	Ala	Glu	Asp	Ala	Glu	Lys	Ile	Gly	Glu		
			170						175					180			
gcc	acc	cgc	aat	gtt	cac	act	gct	ctt	gca	tcg	gcc	ttc	cct	act	cgg	691	
Ala	Thr	Arg	Asn	Val	His	Thr	Ala	Leu	Ala	Ser	Ala	Phe	Pro	Thr	Arg		
			185					190					195				
gta	gtt	ccc	gta	gaa	gca	ctc	gcc	gat	gag	ctc	act	acc	cgc	ctt	aat	739	
Val	Val	Pro	Val	Glu	Ala	Leu	Ala	Asp	Ala	Leu	Thr	Thr	Arg	Leu	Asn		
		200					205					210					
gaa	cta	atc	tcc	caa	gca	ccc	gaa	atc	gcc	cgc	ttc	aaa	gaa	gca	gcc	787	
Glu	Leu	Ile	Ser	Gln	Ala	Pro	Glu	Ile	Ala	Arg	Phe	Lys	Glu	Ala	Ala		
	215					220					225						
atc	gac	ctc	tac	caa	tcg	ttg	gaa	ggc	gaa	gcc	cac	atc	caa	cgc	atc	835	
Ile	Asp	Leu	Tyr	Gln	Ser	Leu	Glu	Gly	Glu	Ala	His	Ile	Gln	Arg	Ile		
	230				235					240					245		
cac	ggg	gac	ctc	cac	ttg	ggg	cag	ctc	atc	aaa	acc	ccc	gaa	cgc	tac	883	
His	Gly	Asp	Leu	His	Leu	Gly	Gln	Leu	Ile	Lys	Thr	Pro	Glu	Arg	Tyr		
			250					255						260			
atc	ctc	atc	gat	ttc	gaa	ggc	gaa	cct	gcc	cgc	cca	ctt	aat	caa	cga	931	
Ile	Leu	Ile	Asp	Phe	Glu	Gly	Glu	Pro	Ala	Arg	Pro	Leu	Asn	Gln	Arg		

265 270 275  
 cgc ctc ccc gac tct ccc ctg aaa gat ctc gcc ggc atc atc aga tcc 979  
 Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala Gly Ile Ile Arg Ser  
 280 285 290  
 atc gac tac gca gcc tac ttc gac ggc gaa cac acc caa tgg gcc aac  
 1027  
 Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His Thr Gln Trp Ala Asn  
 295 300 305  
 gaa gcc acc gcg cta ttc ctc gac ggc tac gga tca att gaa gac caa  
 1075  
 Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly Ser Ile Glu Asp Gln  
 310 315 320 325  
 gaa ctc ctc aat gcc tac att ctg gac aag gcg ttg tac gag gtt gcc  
 1123  
 Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala Leu Tyr Glu Val Ala  
 330 335 340  
 tat gaa ata aac aac cgc ccc gac tgg gtg aaa atc cca ctc gag gcg  
 1171  
 Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys Ile Pro Leu Glu Ala  
 345 350 355  
 gtc gaa agg ctt cta gac tagttagtta ctctgcgtca aac  
 1212  
 Val Glu Arg Leu Leu Asp  
 360

&lt;210&gt; 1156

&lt;211&gt; 363

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 1156

Met Ser Ile Gly Gln His Ile Ile Thr Glu Arg Phe Tyr Gly Ala Lys  
 1 5 10 15  
 Ser His Thr Ile Asp Asn Val Asp Ile Val Leu Ser Arg Glu Cys Gly  
 20 25 30  
 Glu Asn Thr Leu Ala Val Val Arg Ile Asn Asn Ala Leu Tyr Gln Leu  
 35 40 45  
 Leu Val Asn Asp Asp Gly Lys Asp Val Leu Asn Asp His Val Glu Glu  
 50 55 60  
 Val Gly Ala Ser Phe Gly Ala Trp Thr Gly Ser Ser Ala Phe Pro Ile  
 65 70 75 80  
 Gly Pro Phe Thr Pro Leu Gly Thr Glu Gln Ser Asn Ser Ser Phe Ile  
 85 90 95  
 Thr Ala Asp Asn Lys Ala Ile Val Lys Tyr Phe Arg Lys Leu Glu Ser  
 100 105 110  
 Gly Gln Asn Pro Asp Val Glu Leu Ile Ser Lys Ile Ser Ser Cys Pro  
 115 120 125

Asn Ile Ala Pro Ile Leu Gly Phe Ser Ser Ala Glu Ile Ser Gly Ala  
 130 135 140  
 Asn Tyr Thr Leu Val Met Ala Gln Gln Tyr Val Pro Gly Leu Asp Gly  
 145 150 155 160  
 Trp Ser His Ala Leu Thr Thr Thr Ser Gly Ser Phe Ala Glu Asp Ala  
 165 170 175  
 Glu Lys Ile Gly Glu Ala Thr Arg Asn Val His Thr Ala Leu Ala Ser  
 180 185 190  
 Ala Phe Pro Thr Arg Val Val Pro Val Glu Ala Leu Ala Asp Ala Leu  
 195 200 205  
 Thr Thr Arg Leu Asn Glu Leu Ile Ser Gln Ala Pro Glu Ile Ala Arg  
 210 215 220  
 Phe Lys Glu Ala Ala Ile Asp Leu Tyr Gln Ser Leu Glu Gly Glu Ala  
 225 230 235 240  
 His Ile Gln Arg Ile His Gly Asp Leu His Leu Gly Gln Leu Ile Lys  
 245 250 255  
 Thr Pro Glu Arg Tyr Ile Leu Ile Asp Phe Glu Gly Glu Pro Ala Arg  
 260 265 270  
 Pro Leu Asn Gln Arg Arg Leu Pro Asp Ser Pro Leu Lys Asp Leu Ala  
 275 280 285  
 Gly Ile Ile Arg Ser Ile Asp Tyr Ala Ala Tyr Phe Asp Gly Glu His  
 290 295 300  
 Thr Gln Trp Ala Asn Glu Ala Thr Ala Leu Phe Leu Asp Gly Tyr Gly  
 305 310 315 320  
 Ser Ile Glu Asp Gln Glu Leu Leu Asn Ala Tyr Ile Leu Asp Lys Ala  
 325 330 335  
 Leu Tyr Glu Val Ala Tyr Glu Ile Asn Asn Arg Pro Asp Trp Val Lys  
 340 345 350  
 Ile Pro Leu Glu Ala Val Glu Arg Leu Leu Asp  
 355 360